



FT Misc-difference 207 /note= "encoded by TYG"  
XX  
PN WO200122922-A2.  
XX  
PD 05-APR-2001.  
XX  
XX 27-SEP-2000; 2000WO-US026619.  
XX  
XX 27-SEP-1999; 99US-0156194P.  
PR 31-MAY-2000; 2000US-0208684P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Meares C, Chmura A;  
PI WPI; 2001-244971/25.  
XX N-PSDB; AAF30633.  
XX  
XX Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly cancer.  
XX  
XX Disclosure; Fig 12; 100pp; English.  
XX  
XX The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The reactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain variable region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C mutation. As an example of the method of the invention, rational computer-aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a human/mouse chimeric Fab fragment that could be expressed in Escherichia coli, and the synthesis and screening of benzyl-EDTA chelates carrying weakly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site-directed mutagenesis of a nucleic acid encoding the wild-type of the anti-chelate antibody

QY 1 RSAAVTQSALTSTSGETVTLTCRSSIGAVTTSYANVWVQKPDHLFTGLIGGTNNRAGP 60  
Db 1 RSAAVTQSALTSTSGETVTLTCRSSIGAVTTSYANVWVQKPDHLFTGLIGGTNNRAGP 60  
QY 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVFGGGTKLVLSRTVAAPSVF 120  
Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVFGGGTKLVLSRTVAAPSVF 120  
QY 121 IFPPSDEQLKSGTASVVCLLANNFYPREAKVQWVDNALQSGNSQBSVTEQDSKSTYSL 180  
Db 121 IFPPSDEQLKSGTASVVCLLANNFYPREAKVQWVDNALQSGNSQBSVTEQDSKSTYSL 180  
QY 181 STLTLTKADYEHKHYACEVTHQGLSXPVTKSFNRGEC 218  
Db 181 STLTLTKADYEHKHYACEVTHQGLSXPVTKSFNRGEC 218

RESULT 2  
AAB20359  
ID AAB20359 standard; protein; 218 AA.  
XX  
XX AAB20359;  
XX  
XX 11-JUN-2001 (first entry)  
XX  
XX Anti-chelate antibody CHA255 light chain.  
DE  
XX Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
KW cancer; therapy.  
XX  
XX Mus musculus.  
OS  
XX  
XX Key Location/Qualifiers  
FH Region 1. .23  
FT /label= FR1  
FT /note= "framework region 1"  
FT  
FT Region 24. .37  
FT /label= CDR1  
FT /note= "complementarity determining region 1"  
FT Region 38. .52  
FT /label= FR2  
FT /note= "framework region 2"  
FT Region 53. .59  
FT /label= CDR2  
FT /note= "complementarity determining region 2"  
FT Region 60. .92  
FT /label= FR3  
FT /note= "framework region 3"  
FT Region 93. .100  
FT /label= CDR3  
FT /note= "complementarity determining region 3"  
FT Misc-difference 100  
FT /note= "encoded by GTR"  
FT Region 101. .131  
FT /label= FR4  
FT /note= "framework region 4"  
FT Misc-difference 112  
FT /note= "encoded by CGW"  
FT Misc-difference 113  
FT /note= "encoded by ACK"  
FT Misc-difference 206  
FT /note= "encoded by AGY"  
FT Misc-difference 207  
FT /note= "encoded by TYG"  
XX  
XX WO200122922-A2.  
XX  
XX 05-APR-2001.  
XX  
XX 27-SEP-2000; 2000WO-US026619.  
XX  
XX 27-SEP-1999; 99US-0156194P.  
PR 31-MAY-2000; 2000US-0208684P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Meares C, Chmura A;  
PI WPI; 2001-244971/25.  
XX N-PSDB; AAF30633.  
XX  
XX Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly cancer.  
XX  
XX Disclosure; Fig 13; 100pp; English.  
XX  
XX The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a

CC complementarity determining region (CDR) that specifically binds to a  
 CC metal chelate against which the wild-type antibody is raised. The  
 CC reactive site of the mutant antibody is in a position proximate to or  
 CC within the CDR, such that the chelate and the antibody are able to form a  
 CC covalent bond. The present sequence is that of the light chain of anti-  
 CC indium-EDTA monoclonal antibody CHA255. As an example of the method of  
 CC the invention, rational computer-aided design was used to develop an  
 CC indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was  
 CC to allow the chelate to bind non-covalently to CHA255 bound to a tumour  
 CC and then to covalently attach the chelate to the antibody, thereby  
 CC trapping it at the tumour site. This involved cloning the variable  
 CC domains of CHA255 to construct a human/mouse chimeric Fab fragment that  
 CC could be expressed in Escherichia coli, and the synthesis and screening  
 CC of benzyl-EDTA chelates carrying weakly electrophilic groups capable of  
 CC conjugation of the antibody in vivo. This Fab can be conjugated to a  
 CC targeting moiety when desired. A reactive site was incorporated into the  
 CC antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the  
 CC light chain, near the region of the antibody to which the chelate bound.  
 CC This was accomplished by site-directed mutagenesis of a nucleic acid  
 CC encoding the wild-type of the anti-chelate antibody  
 CC  
 XX Sequence 218 AA;

Query Match 98.8%; Score 1118; DB 4; Length 218;  
 Best Local Similarity 99.5%; Pred. No. 6 4e-79;  
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RSVAVTQESALTTSPGTVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRAG 60  
 Db 1 RSVAVTQESALTTSPGTVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRAG 60  
 QY 61 VPARFSGSLIGDKAALTITCAQTEDEARFYCALWYSLWVFGGDKLTVLSRTVAAPSVF 120  
 Db 61 VPARFSGSLIGDKAALTITCAQTEDEARFYCALWYSLWVFGGDKLTVLSRTVAAPSVF 120  
 QY 121 IFPPSDQLKSGTASVVCLLNNFYPRKAVQWVDNALQSGNSQESVTEQDSKDSITYLS 180  
 Db 121 IFPPSDQLKSGTASVVCLLNNFYPRKAVQWVDNALQSGNSQESVTEQDSKDSITYLS 180  
 QY 181 STLTLSKADYEKKHYACEVTHQGLSXPTKSFNRGEC 218  
 Db 181 STLTLSKADYEKKHYACEVTHQGLSXPTKSFNRGEC 218

RESULT 3  
 AAB20360  
 ID AAB20360 standard; protein; 218 AA.  
 AC AAB20360;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Anti-chelate antibody CHA255 light chain mutant S95C.  
 XX  
 KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
 KW cancer; therapy; mutant; mutein.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Region 1..23  
 FT /label= FR1  
 FT /note= "framework region 1"  
 FT Region 24..37  
 FT /label= CDR1  
 FT /note= "complementarity determining region 1"  
 FT Region 38..52  
 FT /label= FR2  
 FT /note= "framework region 2"  
 FT Region 53..59  
 FT /label= CDR2  
 FT /note= "complementarity determining region 2"

FT Region 60..92  
 FT /label= FR3  
 FT /note= "framework region 3"  
 FT Region 93..100  
 FT /label= CDR3  
 FT /note= "complementarity determining region 3"  
 FT Misc-difference 95  
 FT /note= "replaces Ser of wild-type sequence"  
 FT Misc-difference 100  
 FT /note= "encoded by GTR"  
 FT Region 101..131  
 FT /label= FR4  
 FT /note= "framework region 4"  
 FT Misc-difference 112  
 FT /note= "encoded by CGW"  
 FT Misc-difference 113  
 FT /note= "encoded by ACK"  
 FT Misc-difference 206  
 FT /note= "encoded by AGY"  
 FT Misc-difference 207  
 FT /note= "encoded by TYG"  
 XX  
 XX WO200122922-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 XX 27-SEP-2000; 2000WO-US026619.  
 XX  
 XX 27-SEP-1999; 99US-0156194P.  
 PR 31-MAY-2000; 2000US-0208684P.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 PI Hearses C, Chmura A;  
 XX  
 DR WPI; 2001-244971/25.  
 DR N-PSDB; AAF30635.  
 XX  
 XX Nucleic acid encoding a mutant antibody comprising a reactive site that  
 XX specifically binds to a metal chelate useful as analytical agents and in  
 XX clinical diagnosis, as well as in the treatment of disease, particularly  
 XX cancer.  
 XX  
 PS Disclosure; Fig 14; 100pp; English.  
 XX  
 CC The invention provides a mutant antibody comprising a reactive site that  
 CC is not present in the wild-type of the antibody. The antibody also has a  
 CC complementarity determining region (CDR) that specifically binds to a  
 CC metal chelate against which the wild-type antibody is raised. The  
 CC reactive site of the mutant antibody is in a position proximate to or  
 CC within the CDR, such that the chelate and the antibody are able to form a  
 CC covalent bond. The present sequence is that of the light chain variable  
 CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C  
 CC mutation. As an example of the method of the invention, rational computer  
 CC -aided design was used to develop an indium-EDTA chelate to covalently  
 CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-  
 CC covalently to CHA255 bound to a tumour and then to covalently attach the  
 CC chelate to the antibody, thereby trapping it at the tumour site. This  
 CC involved cloning the variable domains of CHA255 to construct a  
 CC human/mouse chimeric Fab fragment that could be expressed in Escherichia  
 CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying  
 CC weakly electrophilic groups capable of conjugation of the antibody in  
 CC vivo. This Fab can be conjugated to a targeting moiety when desired. A  
 CC reactive site was incorporated into the antibody by engineering a Cys  
 CC residue at location Asn-96 or Ser-95 of the light chain, near the region  
 CC of the antibody to which the chelate bound. This was accomplished by site  
 CC -directed mutagenesis of a nucleic acid encoding the wild-type of the  
 CC anti-chelate antibody  
 XX  
 SQ Sequence 218 AA;  
 Query Match 98.3%; Score 1113; DB 4; Length 218;  
 Best Local Similarity 99.1%; Pred. No. 1.6e-78;





PA (REGC ) UNIV CALIFORNIA.  
XX Meares C, Corneillie T;  
XX WPI; 2004-580725/56.  
DR N-PSDB; ADQ98055.  
XX Novel mutant antibody comprising reactive site not present in wild-type  
PT of antibody and antigen recognition domain that recognizes macrocyclic  
PT metal chelate having four nitrogen atoms, useful for treating cancer or  
PT autoimmune diseases.  
XX Claim 41; SEQ ID NO 28; 208pp; English.  
XX This invention relates to multi-functional antibodies that recognise  
CC chelating agents and metal chelates, particularly macrocyclic metal  
CC chelates. Specifically, it refers to an antibody that comprises a metal  
CC chelate bound to an antigen recognition domain, where the metal chelate  
CC has a reactive functional group of complementary reactivity to the  
CC reactive site of the antibody. This reactive site is the side chain of a  
CC naturally occurring amino acid e.g. the -SH group side chain of a  
CC cysteine residue (not present in the wild type) which can be used to form  
CC a covalent bond between the reactive site of the antibody and the  
CC reactive functional group of the metal chelate. The present invention  
CC describes using these antibodies for in vivo imaging where the antibody  
CC comprises a targeting moiety that binds specifically to a cell via a cell  
CC surface receptor or antigen thus forming a cell-mutant antibody complex.  
CC On addition of the metal chelate, a cell-antibody-metal chelate complex  
CC is formed that can be detected using emission tomography, magnetic  
CC resonance imaging, lanthanide luminescence, gamma-emissions or single  
CC photon emission tomography (SPET). As such, this method is useful for  
CC treating a subject with cancer and pharmaceutical compositions exhibit  
CC cytostatic and immunosuppressive activities. This polypeptide sequence is  
CC the chimeric mutant N53C murine antibody 2D12.5 variable light chain  
CC protein fused to the human anti-tetanus toxin antibody kappa light chain  
CC constant region of the invention.  
XX Sequence 218 AA;  
SQ  
Query Match 95.2%; Score 1078; DB 8; Length 218;  
Best Local Similarity 95.9%; Pred. No. 8.2e-76;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 RSAVVTQESALTSPTGETVTLTCRSSIGAVTTSNYANWQEKDPDHLFTGLIGTNNRPPG 60  
DB 1 RSAVVTQESALTSPTGETVTLTCRSSIGAVTTSNYANWQEKDPDHLFTGLIGTNNRPPG 60  
QY 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWVFGGKTLTVLSRTVAAPSVF 120  
DB 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWVFGGKTLTVLSRTVAAPSVF 120  
QY 121 IFPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180  
DB 121 IFPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180  
QY 181 STLTLSKADYKHKVYACEVTHOGLSXPTVTKSFNRGEC 218  
DB 181 STLTLSKADYKHKVYACEVTHOGLSXPTVTKSFNRGEC 218  
RESULT 6  
ADR23362  
ID ADR23362 standard; protein; 215 AA.  
XX ADR23362;  
AC ADR23362;  
XX 04-NOV-2004 (first entry)  
XX Human CD72-targeted IgG1 light chain.  
XX Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;  
XX immunosuppressive; cancer; autoimmune disease; gene therapy.  
XX

OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Region 1..109  
FT /label= V\_region  
FT Region 110..215  
FT /label= C\_region  
XX WO2004067569-A1.  
PN 12-AUG-2004.  
XX 27-JAN-2003; 2003WO-EP050004.  
XX 27-JAN-2003; 2003WO-EP050004.  
PR (CRUC-) CRUCELL HOLLAND BV.  
PA Bakker ABH, Mariissen WE;  
PI WPI; 2004-580978/56.  
DR N-PSDB; ADR23361.  
XX New internalizing human binding molecules capable of specifically binding  
PT to CD72, useful for diagnosing and/or treating B-cell associated  
PT diseases, such as cancer or autoimmune disorders.  
XX Example 5; SEQ ID NO 54; 174pp; English.  
XX The present sequence is the protein sequence of the light chain of human  
CC IgG1 antibody 025, which specifically recognises human B cell associated  
CC antigen CD72. An scFv ADR23324 selected from an antibody phage display  
CC library was shown to specifically recognise the human CD72 receptor. The  
CC scFv was cloned in IGG expression vector C01 using primers designed to  
CC restore complete human frameworks, thereby generating antibody 025. Such  
CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used  
CC as internalising human binding molecules of the invention. These  
CC internalising human binding molecules are capable of (specifically)  
CC binding to CD72 or its antigenic determinant, and preferably bind to CD72  
CC associated with cells. Upon binding to CD72 present on the surface of  
CC target cells, the binding molecules internalise. In addition to the  
CC internalising human binding molecules, the invention provides  
CC immunocjugates comprising an internalising human binding molecule and a  
CC tag (toxic substance, radioactive substance, liposome and/or enzyme),  
CC nucleic acids encoding these, and compositions comprising them. The  
CC internalising human binding molecule, immunocjugate, nucleic acid  
CC molecule or composition can be used in the diagnosis and/or treatment of  
CC a B cell associated disorder or disease, especially a B cell associated  
CC cancer and B cell associated autoimmune disorder (claimed).  
XX Sequence 215 AA;  
SQ  
Query Match 68.6%; Score 776; DB 8; Length 215;  
Best Local Similarity 73.5%; Pred. No. 2.4e-52;  
Matches 161; Conservative 16; Mismatches 36; Indels 6; Gaps 3;  
QY 2 SAVVTQESALTSPTGETVTLTCRSSIGAVTTSNYANWQEKDPDHLFTGLIGTNNRPPG 61  
DB 1 SSELTDPAVSVVALGQTVRITCO---GDSLSRTYASWYQKPKQAPVLVIYGNRPSGI 57  
QY 62 PARFSGSLIGDKAALTITGAQTEDEARYFCALWYSC--LWVFGGKTLTVLSRTVAAPSV 119  
DB 58 PDRFSGSSSGNTASLTITGAQDEADYYCNSRDSGNNHVVFGGKTLTVLG-TVAAPSV 116  
QY 120 FIFPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 179  
DB 117 FIFPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176  
QY 180 SSSLTSLKADYKHKVYACEVTHOGLSXPTVTKSFNRGEC 218  
DB 177 SSSLTSLKADYKHKVYACEVTHOGLSXPTVTKSFNRGEC 215

## RESULT 7

AAW82740  
ID AAW82740 standard; protein; 235 AA.

XX AC AAW82740;

XX DT 10-MAY-1999 (first entry)

XX DE Plasmid pNG3/ASB7VK-HuCK-NEO protein.

XX KW Conjugate; cell targeting; cytotoxic drug; prodrug therapy system;  
KW prodrug-converting enzyme; cell surface antigen; treatment; cancer;  
KW inflammation; rheumatoid arthritis; antibody.

XX OS Synthetic.

XX PN WO9851787-A2.

XX PD 19-NOV-1998.

XX PF 05-MAY-1998; 98WO-GB001294.

XX PR 10-MAY-1997; 97GB-00009421.

XX PA (ZENE ) ZENECA LTD.

XX PI Emery SC, Blakey DC;

XX DR WPI; 1999-059700/05.

XX DR N-PSDB; AAV72047.

XX PT New gene construct expressing conjugate of targeting agent and prodrug-  
PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
PT drug in vivo, especially for treatment of cancer.

XX PS Example 1E; Page 70; 100pp; English.

XX CC This sequence is used in a method for obtaining a novel gene construct  
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
CC targeting group (I) and a heterologous prodrug-converting enzyme (II),  
CC and (B) is directed to leave the cell for selective localisation at a  
CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
CC site, then administration of (III) is used for targeted release of  
CC cytotoxic drug, specifically for treating cancer but also inflammation  
CC such as rheumatoid arthritis. In situ generation of the targeting  
CC antibody increases selectivity, reducing side effects at normal tissue.  
CC The method is applicable to any antibody-directed enzyme prodrug therapy  
CC system

XX SQ Sequence 235 AA;

Query Match 67.0%; Score 759; DB 2; Length 235;

Best Local Similarity 72.2%; Pred. No. 5.5e-51;

Matches 156; Conservative 15; Mismatches 39; Indels 6; Gaps 3;

QY 4 VVTQESA-LTTPSGETVTLTCRSSIGAVTTSNYANWVOEKPDHLFTGLIGTNNRACGPV 62

DB 25 VLSQSFAILSASPGKVTMTCRAS----SSVTYIHWOQKPGSPKSIYATSNLASCVP 80

QY 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYSCLVWFGGKTLTVLSRTVAAPSVPFIF 122

DB 81 ARFSGSGSGTSYSLTISRVEADAATYTCQHWSSKPPFTFGGKTKLEI-KRTVAAPSVPFIF 139

QY 123 PPSDEQLKSGTASVVCLNNFYFPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 182

DB 140 PPSDEQLKSGTASVVCLNNFYFPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 199

QY 193 LTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218

DB 200 LTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 235

## RESULT 8

AAE27925

ID AAE27925 standard; protein; 235 AA.

XX AC AAE27925;

XX DT 27-DEC-2002 (first entry)

XX DE Human C2B8 antibody light chain protein.

XX KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;  
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;  
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.

XX OS Homo sapiens.

XX PN WO200260955-A2.

XX PD 08-AUG-2002.

XX PF 29-JAN-2002; 2002WO-US002373.

XX PR 29-JAN-2001; 2001US-0264318P.

XX PR 16-NOV-2001; 2001US-0331481P.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Braslawsky GR, Hanna N, Chinn P;

XX DR WPI; 2002-698547/75.

XX DR N-PSDB; AAD45754.

XX PT Novel domain deleted CC49 antibody reactive with tumor associated antigen  
PT -72, or C2B8 antibody reactive with CD20, useful for treating  
PT myelosuppressed patient suffering from a neoplastic disorder.

XX PS Example 1; Fig 3B; 74pp; English.

XX CC The present invention relates to domain deleted CC49 or C2B8 antibodies.  
CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain  
CC deleted sequence in which CH2 domain has been deleted and are reactive  
CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive  
CC with CD20 and comprise a heavy chain having a sequence of a derived  
CC domain deleted C2B8 construct where the CH2 domain has been deleted.  
CC Sequences of the invention are useful for imaging a neoplasm. They are  
CC also useful for treating myelosuppressed patients suffering from  
CC neoplastic disorder such as haematologic neoplasm, preferably non-  
CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat  
CC neoplastic disorder, colon cancer and haematologic malignancy. They are  
CC useful for reducing tumour size, inhibiting tumour growth and/or  
CC prolonging the survival time of tumour-bearing animals and for treating  
CC tumours. The present sequence is human C2B8 light chain protein. This  
CC sequence is used in the exemplification of the invention

XX SQ Sequence 235 AA;

Query Match 66.7%; Score 755.5; DB 5; Length 235;

Best Local Similarity 70.5%; Pred. No. 1e-50;

Matches 155; Conservative 16; Mismatches 42; Indels 7; Gaps 3;

QY 1 RSAAVVTQES--ALTTPSGETVTLTCRSSIGAVTTSNYANWVOEKPDHLFTGLIGTNNRA 58

DB 21 RQQIVLSQSFAILSASPGKVTMTCRAS----SSVTYIHWOQKPGSPKSIYATSNLA 76

QY 59 PGVPAFSGSLIGDKAALITGAQTEDEARYFCALWYSCLVWFGGKTLTVLSRTVAAPS 118

DB 77 SGVPVRFSGSGTSYSLTISRVEADAATYTCQWTSNPPTFGGKTKLEI-KRTVAAPS 135

QY 119 VFIFPPSDEQLKSGTASVVCLNNFYFPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 178

DB 136 VFIFPPSDEQLKSGTASVVCLNNFYFPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 195

QY 179 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218

Db 196 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 235

RESULT 9  
ABB82834  
ID ABB82834 standard; protein; 235 AA.  
XX ABB82834;  
XX  
XX 31-MAR-2003 (first entry)  
XX Antibody C2B8 light chain.  
XX  
XX C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;  
KW vstropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;  
KW thymimetic; hepatotropic; haemostatic; antileptotic; antibacterial;  
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antilucer;  
KW dermatological; immunosuppressive; antiinflammatory.  
XX  
XX Homo sapiens.  
OS  
XX WO200296948-A2.  
PN  
XX 05-DEC-2002.  
PD  
XX  
XX 29-JAN-2002; 2002WO-US002374.  
PF  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
PR  
XX 16-NOV-2001; 2001US-0331481P.  
PR  
XX 21-DEC-2001; 2001US-0341858P.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
PA  
XX  
XX Braslowsky GR, Hanna N, Chinn P, Hariharan K;  
PI  
XX WPI; 2003-140446/13.  
DR  
XX N-PSDB; ABZ24018.  
DR  
XX  
XX Novel dimeric antibody useful for treating immune disorder and neoplastic  
PT disorder, has several non-covalently associated monomeric subunits.  
PT  
XX  
XX Example 1; Fig 3B; 78pp; English.  
PS  
XX  
XX The invention relates to a dimeric antibody (I) comprising several  
CC monomeric subunits, where the monomeric subunits are non-covalently  
CC associated. (I) is useful for treating a disorder, especially immune  
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
CC lymphoplasmacytoid lymphoma (IPL), mantle cell lymphoma (MCL), follicular  
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a  
CC detailed description of the various uses of (I)). The present sequence  
CC represents the antibody C2B8 light chain  
XX  
XX Sequence 235 AA;  
XX  
Query Match 66.7%; Score 755.5; DB 6; Length 235;  
Best Local Similarity 70.5%; Pred. No. 1e-50;  
Matches 155; Conservative 16; Mismatches 42; Indels 7; Gaps 3;  
XX

Qy 1 R5AVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNANVWQEKPDHLFTGLIGTNNRA 58  
Db 21 RQIVLSOSPAILSGPGEKVTMTCRAS----SSVSIHWFQKPGSPKWIATSNLA 76  
Qy 59 PGVPARPGSSGLIGDKAALITGAQTEDEARYFCALWYSCLVWFGGKTLTVLSRTVAAPS 118  
Db 77 SGVPVRFGSGSGTSYSLITISRVEAEDAATYCCQWTSNPPTFGGKLEI-KRTVAAPS 135

Qy 119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 178  
Db 136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 195  
Qy 179 LSSTLTLSKADYKHKVYACEVTHQGLSKXPVTKSNRGE 218  
Db 196 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 235

RESULT 10  
ADL92471  
ID ADL92471 standard; protein; 213 AA.  
XX  
XX ADL92471;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
XX Antibody "Rituximab" light chain sequence.  
XX  
XX cytostatic; antiinflammatory; cardiovascular; gene therapy; antibody; Fc;  
KW agriculture; industrial application.  
KW  
XX Homo sapiens.  
OS  
XX WO2004029207-A2.  
PN  
XX 08-APR-2004.  
PD  
XX  
XX 26-SEP-2003; 2003WO-US030249.  
PF  
XX  
XX 27-SEP-2002; 2002US-0414433P.  
PR  
XX 23-JAN-2003; 2003US-042301P.  
PR  
XX 02-MAY-2003; 2003US-0467606P.  
PR  
XX 12-JUN-2003; 2003US-0477839P.  
XX  
XX (XENC-) XENCOR.  
XX  
XX Lazar GA, Chirino AJ, Dang W, Desjarlais JR, Doberstein SK;  
PI  
XX Hayes RJ, Karli SB, Vafa O;  
XX  
XX WPI; 2004-316096/29.  
XX  
XX New optimized Fc variant antibody useful for diagnosing or treating  
PT diseases (e.g. cancer, inflammation or cardiovascular diseases), in  
PT research and in agricultural or industrial applications.  
XX  
XX Example 12; Fig 31a; 192pp; English.  
XX  
XX The invention relates to an antibody comprising an Fc variant portion  
CC having an amino acid modification in the Fc region of the parent Fc  
CC polypeptide, where the Fc variant modulates binding to an Fc-gamma-R  
CC compared to the parent Fc polypeptide. The antibody may also be used in  
CC research and in agricultural or industrial applications. This sequence  
CC corresponds to the light chain of the antibody "Rituximab" as an example  
CC of an antibody of the invention.  
XX  
XX Sequence 213 AA;  
XX  
Query Match 66.7%; Score 755; DB 8; Length 213;  
Best Local Similarity 71.8%; Pred. No. 1e-50;  
Matches 155; Conservative 16; Mismatches 39; Indels 6; Gaps 3;  
XX

Qy 4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNANVWQEKPDHLFTGLIGTNNRAGVP 62  
Db 3 VLQSOPAILSGPGEKVTMTCRAS----SSVSIHWFQKPGSPKWIATSNLASEVP 58  
Qy 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYSCLVWFGGKTLTVLSRTVAAPSVP 122  
Db 59 VRFGSGSGTSYSLITISRVEAEDAATYCCQWTSNPPTFGGKLEI-KRTVAAPSVP 117  
Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 182  
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 177

—

CC and aplastic anaemia. They are also useful for inducing hyper-cross-  
CC linking of membrane antigens and for the preferential killing of selected  
CC cell populations. (Updated on 12-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 235 AA;

Query Match 66.3%; Score 750.5; DB 3; Length 235;  
Best Local Similarity 70.0%; Pred. No. 2.5e-50;  
Matches 154; Conservative 16; Mismatches 43; Indels 7; Gaps 3;

QY 1 RSVAVTOES--ALTTSPGETVLTCSRSSIGAVTTSYANWVQEKDPDHLFTGLIGTNNRA 58  
DB 21 RQIVLSQSPALSLSPGKVTMTCRAS-----SSVSIHWFQKPGSPKRWIYATSNLA 76  
QY 59 PGVPRFSGSLIGDKAALTITGAQTEDEARYFCALWYCLWVFGGTKLTVLSRTVAAPS 118  
DB 77 SGVPRVRFSGSGTSLTISRVAEDAATYYCQWTSNPPTFFGGGAKLEI-KRTVAAPS 135  
QY 119 VFIPPSDQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKSTYS 178  
DB 136 VFIPPSDQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKSTYS 195  
QY 179 LSTLTLSKADYKHKVYACEVTHOGLSXPTKSFNRGEC 218  
DB 196 LSTLTLSKADYKHKVYACEVTHOGLSXPTKSFNRGEC 235

RESULT 13  
AAO14066  
ID AAO14066 standard; protein; 234 AA.  
XX  
AC AAO14066;  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Light chain protein of the monoclonal antibody from clone JA.  
XX  
KW HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;  
KW human monoclonal rabies virus neutralising antibody; immunoglobulin;  
KW light chain; central nervous system; CNS; prophylactic therapy; clone JA.  
XX  
OS Homo sapiens.  
XX WO200188132-A2.  
XX  
XX 22-NOV-2001.  
XX  
XX 04-MAY-2001; 2001WO-US014468.  
XX  
XX 16-MAY-2000; 2000US-0204518P.  
XX  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
XX Hooper DC, Dietzschold B;  
XX  
XX WPI; 2002-062381/08.  
XX N-PSDB; AAK98702.  
XX  
XX Novel isolated human monoclonal rabies virus neutralizing antibody useful  
XX for treating individual exposed to rabies virus and for preventing spread  
XX of rabies virus to central nervous system.  
XX  
XX Claim 4; Page 24-25; 25pp; English.  
XX  
XX This sequence represents the light chain protein of the monoclonal  
XX antibody from clone JA. The invention relates to an isolated human  
XX monoclonal rabies virus neutralising antibody (virucide) derived from  
XX cDNA clones encoding the antibody heavy and light chains expressed in  
XX heterologous expression systems and purified away from deleterious  
XX contaminants. The invention provides a fused gene encoding a chimeric  
XX immunoglobulin light chain and a fused gene encoding a chimeric  
XX immunoglobulin heavy chain. The antibody of the invention is useful for  
XX treating an individual exposed to a rabies virus by administering to the

CC individual a therapeutically effective amount of the antibody, and  
CC preventing a spread of the rabies virus to the central nervous system  
CC (CNS). The antibody of the invention provides a safe and efficacious post  
CC -exposure prophylactic therapy for individuals exposed to a rabies virus  
XX  
SQ Sequence 234 AA;

Query Match 66.2%; Score 749.5; DB 5; Length 234;  
Best Local Similarity 71.8%; Pred. No. 3e-50;  
Matches 155; Conservative 13; Mismatches 43; Indels 5; Gaps 3;

QY 4 VVTQESA-LTTSPGETVLTCSRSSIGAVTTSYANWVQEKDPDHLFTGLIGTNNRAGVP 62  
DB 23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQKPGQAPRLLIYDTSNRATGIP 79  
QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCLWVFGGTKLTVLSRTVAAPSVFIF 122  
DB 80 ARFSGSGGTDTLTLSISLEPEDFAVYVCQQRFNWPTFGGTVKE-FKRTVAAPSVFIF 138  
QY 123 PPSDEQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKSTYSLSST 182  
DB 139 PPSDEQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKSTYSLSST 198  
QY 183 LTLKADYKHKVYACEVTHOGLSXPTKSFNRGEC 218  
DB 199 LTLKADYKHKVYACEVTHOGLSXPTKSFNRGEC 234

RESULT 14  
ABU08018  
ID ABU08018 standard; protein; 234 AA.  
XX  
AC ABU08018;  
XX  
DT 10-MAY-2003 (first entry)  
XX  
DE Human monoclonal rabies virus antibody light chain, clone JH, protein.  
XX  
KW Human; antibody; constant region; monoclonal antibody 57; Mab 57;  
KW variable region; Rabies; neurological disease; infection;  
KW central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;  
KW pathogen; vaccine; virucide; light chain.  
XX  
OS Homo sapiens.  
XX WO2003016501-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 21-AUG-2002; 2002WO-US026584.  
XX  
XX 21-AUG-2001; 2001US-0314023P.  
XX  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
XX Hooper DC, Dietzschold B;  
XX  
XX WPI; 2003-278566/27.  
XX N-PSDB; ABX12856.  
XX  
XX New recombinant antibody comprising a constant region of Mab 57 linked to  
XX a non-Mab 57 variable region, useful for treating an individual exposed  
XX to a pathogen, e.g. rabies infection.  
XX  
XX Example 1; Page 33-34; 38pp; English.  
XX  
XX The invention discloses a recombinant antibody comprising a constant  
XX region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable  
XX region. Rabies is an acute, neurological disease caused by infection of  
XX the central nervous system with the rabies virus, a member of the  
XX Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods  
XX for producing an isolated recombinant antibody by culturing a host cell,  
XX containing a recombinant expression vector comprising the nucleic acid

CC molecule encoding the antibody, and isolating the recombinant antibody  
 CC expressed and treating an individual exposed to a pathogen by  
 CC administering to the individual the recombinant antibody. The recombinant  
 CC antibodies are useful for preventing (vaccine) and treating an individual  
 CC exposed to a pathogen, e.g. rabies infection. They are also useful for  
 CC the qualitative and quantitative determination of the rabies virus. The  
 CC sequences presented are the antibody protein fragments, the nucleic acids  
 CC encoding them or the PCR primers used to construct the recombinant  
 CC expression vector  
 XX  
 SQ Sequence 234 AA;

Query Match 66.2%; Score 749.5; DB 6; Length 234;  
 Best Local Similarity 71.8%; Pred. No. 3e-50; Indels 5; Gaps 3;  
 Matches 155; Conservative 13; Mismatches 43;  
 QY 4 VVTQESA-LTTPSGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRAGVP 62  
 DB 23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQKPGQAPRLLIYDTSNRATGIP 79  
 QY 63 ARFSGSLIGDKAALTTGAQTEDEARYFCALWYSLWVFGGTXLTVLSRTVAAPSVPFIF 122  
 DB 80 ARFSGSGGTDFTLSSISLEPEDFAVYCYQORFNWPTFGQGTKVE-FKRTVAAPSVPFIF 138  
 QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 182  
 DB 139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 198  
 QY 183 LTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218  
 DB 199 LTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 234

## RESULT 15

ADP65776  
 ID ADP65776 standard; protein; 234 AA.  
 XX  
 AC ADP65776;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human monoclonal rabies virus antibody light chain.  
 XX  
 KW Immunoglobulin; Ig; heavy chain; light chain; human;  
 KW monoclonal rabies virus neutralising antibody; rabies virus protein;  
 KW neuronal tissue; antirabies.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003157112-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 21-AUG-2002; 2002US-00225108.  
 XX  
 PR 16-MAY-2000; 2000US-0204519P.  
 PR 04-MAY-2001; 2001US-00848832.  
 PR 21-AUG-2001; 2001US-0314023P.  
 XX  
 PA (HOOP/) HOOPER D C.  
 PA (DIET/) DIETZSCHOLD B.  
 XX  
 PI Hooper DC, Dietzschold B;  
 XX  
 DR WPI; 2003-777974/73.  
 DR N-PSDB; ADP65790.  
 XX  
 PT New isolated nucleic acid molecule encoding a sequence that neutralizes  
 PT an antibody that binds to rabies virus protein, useful for diagnosing,  
 PT preventing or treating infection of pathogens that target neuronal  
 PT tissues, e.g. rabies.  
 XX  
 PS Claim 2; SEQ ID NO 4; 22pp; English.

XX The present invention relates to the isolation of immunoglobulin (Ig)  
 CC heavy and light chains of human monoclonal rabies virus neutralising  
 CC antibody, and the polynucleotide sequences encoding them. The antibody  
 CC specifically binds to a rabies virus protein. Also disclosed is a fused  
 CC gene encoding a chimeric immunoglobulin light or heavy chain comprising a  
 CC first DNA sequence encoding an immunoglobulin light or heavy chain  
 CC variable region of a monoclonal rabies virus neutralising antibody  
 CC produced by a heterohybridoma cell line and a second DNA sequence  
 CC encoding a human light or heavy chain constant region, and methods of  
 CC producing a recombinant antibody. The polynucleotide sequences,  
 CC antibodies and methods are useful for diagnosing, preventing or treating  
 CC an infection of pathogens that target neuronal tissues, particularly  
 CC rabies. The present sequence represents human monoclonal rabies virus  
 CC antibody light chain.  
 XX  
 SQ Sequence 234 AA;

Query Match 66.2%; Score 749.5; DB 7; Length 234;  
 Best Local Similarity 71.8%; Pred. No. 3e-50; Indels 5; Gaps 3;  
 Matches 155; Conservative 13; Mismatches 43;  
 QY 4 VVTQESA-LTTPSGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRAGVP 62  
 DB 23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQKPGQAPRLLIYDTSNRATGIP 79  
 QY 63 ARFSGSLIGDKAALTTGAQTEDEARYFCALWYSLWVFGGTXLTVLSRTVAAPSVPFIF 122  
 DB 80 ARFSGSGGTDFTLSSISLEPEDFAVYCYQORFNWPTFGQGTKVE-FKRTVAAPSVPFIF 138  
 QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 182  
 DB 139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 198  
 QY 183 LTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218  
 DB 199 LTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 234

Search completed: June 7, 2005, 15:54:03  
 Job time : 117.5 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	759	67.0	235	3	US-09-423-439-18	Sequence 18, Appl	
2	751	66.3	220	3	US-08-952-235-1	Sequence 1, Appl	
3	751	66.3	220	4	US-09-669-971-1	Sequence 1, Appl	
4	740	65.4	233	4	US-09-472-087-15	Sequence 15, Appl	
5	740	65.4	233	4	US-09-472-087-67	Sequence 67, Appl	
6	738	65.2	235	4	US-09-011-769A-27	Sequence 27, Appl	
7	735	64.9	213	3	US-08-397-411-12	Sequence 12, Appl	
8	734.5	64.9	491	4	US-10-011-125A-2	Sequence 2, Appl	
9	734	64.8	236	4	US-09-315-926A-79	Sequence 79, Appl	
10	732	64.7	235	4	US-09-472-087-14	Sequence 14, Appl	
11	732	64.7	235	4	US-09-472-087-65	Sequence 65, Appl	
12	730.5	64.5	214	4	US-09-472-087-71	Sequence 71, Appl	
13	730.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl	
14	730.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl	
15	729.5	64.4	234	4	US-09-472-087-17	Sequence 17, Appl	
16	729.5	64.4	234	4	US-09-472-087-69	Sequence 69, Appl	
17	728.5	64.4	224	4	US-09-456-090A-46	Sequence 46, Appl	
18	728.5	64.4	224	4	US-09-453-234-46	Sequence 46, Appl	
19	728.5	64.4	234	4	US-09-740-002-24	Sequence 24, Appl	
20	728	64.3	214	1	US-08-458-516-12	Sequence 12, Appl	
21	727	64.2	233	3	US-09-485-737B-69	Sequence 69, Appl	
22	727	64.2	233	3	US-10-071-485-69	Sequence 69, Appl	
23	726	64.1	235	3	US-09-171-945-17	Sequence 17, Appl	
24	725.5	64.1	224	4	US-09-456-090A-36	Sequence 36, Appl	
25	725.5	64.1	224	4	US-09-453-234-36	Sequence 36, Appl	
26	725.5	64.1	226	4	US-09-456-090A-74	Sequence 74, Appl	
27	725.5	64.1	226	4	US-09-453-234-74	Sequence 74, Appl	

Db 81 ARFSGSGTSYSLTISRVEADAATYYCQHWSSKPPTFGGKLEI-KRTVAAPSVFIP 139  
Qy 123 PPSDQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSST 182  
Db 140 PPSDQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSST 199  
Qy 183 LTLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218  
Db 200 LTLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 235

## RESULT 2

US-08-952-235-1  
; Sequence 1, Application US/08952235  
; Patent No. 6207152  
; GENERAL INFORMATION:  
; APPLICANT: Schwall, Ralph H.  
; APPLICANT: Tabor, Kelly H.  
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
; TITLE OF INVENTION: Antagonists and Uses Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,235  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-952-235-1

Query Match 66.3%; Score 751; DB 3; Length 220;  
Best Local Similarity 71.8%; Pred. No. 9.2e-67;  
Matches 153; Conservative 14; Mismatches 42; Indels 4; Gaps 2;  
Qy 9 SALTTPSGETVTLTCRSSIGAVTTS---NYANWVQEKDPDHLFTGLIGTNNRPAFGVPARF 65  
Db 9 SSLTVSVEKVTVCSSQSLLYTSQKNYLAWYQKPGQPKLLIYWASTRESGVDPDF 68  
Qy 66 SGLSLGDKAALTITGAQTEDEARYFCALWYCLWVFGGKTLTVLSRTVAAPSVFIFPPS 125  
Db 69 TGSQSGTDFLTITTSVKADDLAVYQYQYAYPMTFGGKLEI-KRTVAAPSVFIFPPS 127  
Qy 126 DEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 185  
Db 128 DEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 187  
Qy 186 SKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218  
Db 188 SKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 220

## RESULT 4

US-09-472-087-15  
; Sequence 15, Application US/09472087  
; Patent No. 6682736

## RESULT 3

US-09-669-971-1  
; Sequence 1, Application US/09669971  
; Patent No. 6468529  
; GENERAL INFORMATION:  
; APPLICANT: Schwall, Ralph H.  
; APPLICANT: Tabor, Kelly H.  
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
; TITLE OF INVENTION: Antagonists and Uses Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/669,971  
; FILING DATE: 05-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,235  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-669-971-1

Query Match 66.3%; Score 751; DB 4; Length 220;  
Best Local Similarity 71.8%; Pred. No. 9.2e-67;  
Matches 153; Conservative 14; Mismatches 42; Indels 4; Gaps 2;  
Qy 9 SALTTPSGETVTLTCRSSIGAVTTS---NYANWVQEKDPDHLFTGLIGTNNRPAFGVPARF 65  
Db 9 SSLTVSVEKVTVCSSQSLLYTSQKNYLAWYQKPGQPKLLIYWASTRESGVDPDF 68  
Qy 66 SGLSLGDKAALTITGAQTEDEARYFCALWYCLWVFGGKTLTVLSRTVAAPSVFIFPPS 125  
Db 69 TGSQSGTDFLTITTSVKADDLAVYQYQYAYPMTFGGKLEI-KRTVAAPSVFIFPPS 127  
Qy 126 DEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 185  
Db 128 DEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 187  
Qy 186 SKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218  
Db 188 SKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 220



GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILLEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PF1  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-15

Query Match 65.4%; Score 740; DB 4; Length 233;  
Best Local Similarity 70.4%; Pred. No. 1.2e-65;  
Matches 152; Conservative 18; Mismatches 40; Indels 6; Gaps 3;

QY 4 VVTOE-SALTTSPGETVTLTCRSSIGAVTTSYANVWQKPDHFLTGLIGTNNRAGVVP 62  
Db 23 VLTQSPGTLTSLSPGERATLSCRTSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIP 78

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVFIF 122  
Db 79 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYIGISPTFTGGGTVKEI-KRTVAAPSVFIF 137

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 182  
Db 138 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 197

QY 183 LTLSKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218  
Db 198 LTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGEC 233

RESULT 6  
US-09-011-769A-27  
Sequence 27, Application US/09011769A  
Patent No. 6436691  
GENERAL INFORMATION:  
APPLICANT: SLATER, Anthony M.  
BLAKEY, David C.  
DAVIES, David H.  
HENNAM, John F.  
HENNEQUIN, Laurent F.A.  
MARSHAM, Peter R.  
DOWELL, Robert I.  
TITLE OF INVENTION: Chemical Compounds  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pillsbury Madison & Sutro, LLP  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 1.44 Mb disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,769A  
FILING DATE: 13-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/01975  
FILING DATE: 13-AUG-1996  
APPLICATION NUMBER: GB 9612295.7  
FILING DATE: 12-JUN-1996  
APPLICATION NUMBER: GB 9611019.2  
FILING DATE: 25-MAY-1996  
APPLICATION NUMBER: GB 9516810.0  
FILING DATE: 16-AUG-1995  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-011-769A-27

Query Match 65.2%; Score 738; DB 4; Length 235;  
Best Local Similarity 71.3%; Pred. No. 2e-65;  
Matches 154; Conservative 15; Mismatches 41; Indels 6; Gaps 3;

QY 4 VVTOE-SALTTSPGETVTLTCRSSIGAVTTSYANVWQKPDHFLTGLIGTNNRAGVVP 62  
Db 25 VLTQSPSSLVSIVGDRVTMTCRAS-----SSVTYIHWYQKPGKGLAPKSWIATSNLASGVP 80

GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILLEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PF1  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-15

Query Match 65.4%; Score 740; DB 4; Length 233;  
Best Local Similarity 70.4%; Pred. No. 1.2e-65;  
Matches 152; Conservative 18; Mismatches 40; Indels 6; Gaps 3;

QY 4 VVTOE-SALTTSPGETVTLTCRSSIGAVTTSYANVWQKPDHFLTGLIGTNNRAGVVP 62  
Db 23 VLTQSPGTLTSLSPGERATLSCRTSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIP 78

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVFIF 122  
Db 79 DRFSGSGSGTDFTLTISRLEPEDFAVYVCOQYIGISPTFTGGGTVKEI-KRTVAAPSVFIF 137

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 182  
Db 138 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 197

QY 183 LTLSKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218  
Db 198 LTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGEC 233

RESULT 5  
US-09-472-087-67  
Sequence 67, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILLEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PF1  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 67  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-67

Query Match 65.4%; Score 740; DB 4; Length 233;  
Best Local Similarity 70.4%; Pred. No. 1.2e-65;  
Matches 152; Conservative 18; Mismatches 40; Indels 6; Gaps 3;

Qy 63 ARFSGSLGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVFIF 122  
Db 81 SRFGSGSGTDYTLTISLSQPEDATYYCQHWSKPPFTFGGQTKVEI-KRTVAAPSVFIF 139  
Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSST 182  
Db 140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSST 199  
Qy 183 LTLSKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
Db 200 LTLSKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 235

RESULT 7  
US-08-397-411-12  
; Sequence 12, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tao, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-004901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 213 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-411-12

Query Match 64.9%; Score 735; DB 3; Length 213;  
Best Local Similarity 70.7%; Pred. No. 3.4e-65;  
Matches 152; Conservative 16; Mismatches 41; Indels 6; Gaps 3;

Qy 5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSYANWVQKPDHFLFTGLIGGTNNRAGVPA 63  
Db 4 MTQSPSSLSASVGDRTVITCSAS---SSVSVMWYQQKPKGKPKRLIYDTSKLASGVPS 59  
Qy 64 RFGSGLGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVFIF 123  
Db 60 RFGSGSGTDYTLTISLSQPEDFDITYCQWSSNPPTFGGQTKVEI-KRTVAAPSVFIF 118  
Qy 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSSTL 183

Query Match 64.9%; Score 734.5; DB 4; Length 491;  
Best Local Similarity 70.7%; Pred. No. 1.2e-64;  
Matches 152; Conservative 16; Mismatches 42; Indels 5; Gaps 3;

Qy 5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSYANWVQKPDHFLFTGLIGGTNNRAGVPA 63  
Db 27 LTQSPSSLSASVGDRTVITCSAS---QDISNLYNWYQQKPKGKPKRLIYFTSSLHSGVPS 83  
Qy 64 RFGSGLGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVFIF 123  
Db 84 RFGSGSGTDYTLTISLSQPEDFATYYCQYSTVPMTFGGQTKVEI-KRTVAAPSVFIF 142  
Qy 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSSTL 183  
Db 143 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSSTL 202  
Qy 184 TLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
Db 203 TLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 237

RESULT 9  
US-09-315-926A-79  
; Sequence 79, Application US/09315926A  
; Patent No. 6498027  
; GENERAL INFORMATION:  
; APPLICANT: Es van, Helmut  
; APPLICANT: Havenga, Menzo  
; APPLICANT: Verlinden, Stefan  
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER  
; FILE REFERENCE: 2183-4080US  
; CURRENT APPLICATION NUMBER: US/09/315,926A  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: EP 99201593.3  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: EP 98201693.3  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 79  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

Db 119 PSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSSTL 178  
Qy 184 TLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
Db 179 TLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 213

RESULT 8  
US-10-011-125A-2  
; Sequence 2, Application US/10011125A  
; Patent No. 6828121  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Christina Yu-Ching  
; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
; FILE REFERENCE: P1804R1  
; CURRENT APPLICATION NUMBER: US/10/011,125A  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/256,162  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 2  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
; Patent No. 6828121  
US-10-011-125A-2

Query Match 64.9%; Score 734.5; DB 4; Length 491;  
Best Local Similarity 70.7%; Pred. No. 1.2e-64;  
Matches 152; Conservative 16; Mismatches 42; Indels 5; Gaps 3;

Qy 5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSYANWVQKPDHFLFTGLIGGTNNRAGVPA 63  
Db 27 LTQSPSSLSASVGDRTVITCSAS---QDISNLYNWYQQKPKGKPKRLIYFTSSLHSGVPS 83  
Qy 64 RFGSGLGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVFIF 123  
Db 84 RFGSGSGTDYTLTISLSQPEDFATYYCQYSTVPMTFGGQTKVEI-KRTVAAPSVFIF 142  
Qy 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSSTL 183  
Db 143 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSSTL 202  
Qy 184 TLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
Db 203 TLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 237

RESULT 9  
US-09-315-926A-79  
; Sequence 79, Application US/09315926A  
; Patent No. 6498027  
; GENERAL INFORMATION:  
; APPLICANT: Es van, Helmut  
; APPLICANT: Havenga, Menzo  
; APPLICANT: Verlinden, Stefan  
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER  
; FILE REFERENCE: 2183-4080US  
; CURRENT APPLICATION NUMBER: US/09/315,926A  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: EP 99201593.3  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: EP 98201693.3  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 79  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

```

;
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(236)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79

Query Match      64.8%; Score 734; DB 4; Length 236;
Best Local Similarity 72.6%; Pred. No. 4.9e-65;
Matches 151; Conservative 13; Mismatches 42; Indels 2; Gaps 2;

Qy      11  LTTSPGETVLTCSRSGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPGVDPARRSGSLI 70
Db      31  LSLSPGAGATLSCRAS-QSVSSRNLA-WYQKPGQAPRLLIYGVSNRATGVPDRFSGSGS 88

Qy      71  GDKAALTTTGAQTEDEARYFCALWYSCLVWVFGGTTKLTVLSRTVAAPSVFIPPPSDEQLK 130
Db      89  GADFTLTINLEPEDFAVYCYQYGRSLWTFGGTKVEIKRGTVAAAPSVFIPPPSDEQLK 148

Qy      131  SGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADY 190
Db      149  SGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADY 208

Qy      191  EKHVYACEVTHOGLSPVTKSFNRGEC 218
Db      209  EKHVYACEVTHOGLSPVTKSFNRGEC 236

RESULT 10
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match      64.7%; Score 732; DB 4; Length 235;
Best Local Similarity 69.4%; Pred. No. 7.8e-65;
Matches 150; Conservative 19; Mismatches 43; Indels 4; Gaps 3;

Qy      4  VVTOE-SALTSPGETVLTCSRSGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPGV 62
Db      23  VLTQSPGTLSLSPGERATLSCRAS--QSISSEFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy      63  ARFSGSLIGDKAALTTTGAQTEDEARYFCALWYSCLVWVFGGTTKLTVLSRTVAAPSVFIF 122
Db      81  DRFSGSGSGTDFTLTISRLEPEDFAVYCYQYGTSPWTFGGTKVEI-KRTVAAPSVFIF 139

Qy      123  PPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 182
Db      140  PPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 199

Qy      183  LTLKADYKHKVYACEVTHOGLSPVTKSFNRGEC 218
Db      200  LTLKADYKHKVYACEVTHOGLSPVTKSFNRGEC 235

RESULT 12
US-09-472-087-71
; Sequence 71, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 214
; TYPE: PRT
US-09-472-087-71
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Db      200  LTLKADYKHKVYACEVTHOGLSPVTKSFNRGEC 235

RESULT 11
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      64.7%; Score 732; DB 4; Length 235;
Best Local Similarity 69.4%; Pred. No. 7.8e-65;
Matches 150; Conservative 19; Mismatches 43; Indels 4; Gaps 3;

Qy      4  VVTOE-SALTSPGETVLTCSRSGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPGV 62
Db      23  VLTQSPGTLSLSPGERATLSCRAS--QSISSEFLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy      63  ARFSGSLIGDKAALTTTGAQTEDEARYFCALWYSCLVWVFGGTTKLTVLSRTVAAPSVFIF 122
Db      81  DRFSGSGSGTDFTLTISRLEPEDFAVYCYQYGTSPWTFGGTKVEI-KRTVAAPSVFIF 139

Qy      123  PPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 182
Db      140  PPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 199

Qy      183  LTLKADYKHKVYACEVTHOGLSPVTKSFNRGEC 218
Db      200  LTLKADYKHKVYACEVTHOGLSPVTKSFNRGEC 235

RESULT 12
US-09-472-087-71
; Sequence 71, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 214
; TYPE: PRT
US-09-472-087-71
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; ORGANISM: Homo sapiens
US-09-472-087-71

Query Match      64.5%; Score 730.5; DB 4; Length 214;
Best Local Similarity 69.8%; Pred. No. 9.7e-65;
Matches 150; Conservative 20; Mismatches 40; Indels 5; Gaps 3;

Qy 5 VTQE-SALTTPGTTVLTCSRSGAVTTSNYANWQKPDHLFTGLIGTNNRAPGVP 63
Db 4 MTQSPSSLASVGRVTTTCRAS--QSINSYLDWYQKPGKAPKLLIYAASLSQSGVPS 60
Qy 64 RFSSGLIGDKAALITGAQTEDEARYFCALWYSCILWVFGGKTLTVLSRTVAAPSVPFIP 123
Db 61 RFGSGSGTDFTLTSSLPQDFATYCCQYISTPFTFGPGTKVEI-KRTVAAPSVPFIP 119
Qy 124 PSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTL 183
Db 120 PSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTL 179
Qy 184 LTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218
Db 180 LTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 214

RESULT 13
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Loberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84

Query Match      64.5%; Score 730.5; DB 4; Length 224;
Best Local Similarity 71.2%; Pred. No. 1e-64;
Matches 153; Conservative 15; Mismatches 42; Indels 5; Gaps 3;

Qy 4 VVTQESA-LTTSBGETVLTCSRSGAVTTSNYANWQKPDHLFTGLIGTNNRAPGVP 62
Db 3 VLTQSPATLSLSPGERATLSCRAS--QSVSSYLAWYQQKPGQAPRLIIYDASNRAAGIP 59
Qy 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYSCILWVFGGKTLTVLSRTVAAPSVPFIF 122
Db 60 ARFSGSGSGTDFTLTSSLEPEDFAVYCCQRNNWPLTFGGGTKEI-KRTVAAPSVPFIF 118
Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLST 182
Db 119 PPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLST 178
Qy 183 LTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGE 217
Db 179 LTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGE 213

RESULT 15
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-17

Query Match      64.4%; Score 729.5; DB 4; Length 234;
Best Local Similarity 69.9%; Pred. No. 1.4e-64;
Matches 151; Conservative 17; Mismatches 43; Indels 5; Gaps 3;

Qy 4 VVTQE-SALTTPGTTVLTCSRSGAVTTSNYANWQKPDHLFTGLIGTNNRAPGVP 62
Db 3 VVTQE-SALTTPGTTVLTCSRSGAVTTSNYANWQKPDHLFTGLIGTNNRAPGVP 62
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Db 23 VLTQSPGTLSPGERATLS CRAS---QSVSSYLAWYQOKPGQAPRPLIYGVSSRATGIP 79  
QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGQTKLTVLSRTVAAPSVFIF 122  
Db 80 DRFSGSGSGTDFTLATISRLPEPDAVYQCQYGISPFTFGPGTKVDI-KRTVAAPSVFIF 138  
QY 123 PPSDEOLKSGTASVWCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182  
Db 139 PPSDEOLKSGTASVWCLLNFPYPRKAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 198  
QY 183 LTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218  
Db 199 LTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234

Search completed: June 7, 2005, 16:02:13  
Job time : 30.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 16:00:22 ; Search time 100 Seconds  
(without alignments)  
785.243 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
Sequence: 1 RSAVVTQESALTTSPGETVTLTCSRSSIGAVTTSNYANWVQEKDHLFTGLIGTNNRPPG 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues  
Total number of hits satisfying chosen parameters: 1599520

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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21: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1079	95.3	218	16	US-10-625-047-27
2	1078	95.2	218	16	US-10-625-047-28
3	755.5	66.7	235	16	US-10-723-003-42
4	751	66.3	220	9	US-09-995-693-1
5	751	66.3	220	14	US-10-232-408-1
6	749.5	66.2	234	10	US-09-848-832-4
7	749.5	66.2	234	14	US-10-225-108A-4
8	749.5	66.2	234	15	US-10-461-148-2
9	749	66.2	213	14	US-10-150-475A-8
10	749	66.2	213	16	US-10-704-522-8
11	749	66.2	213	16	US-10-645-215-8
12	747	66.0	213	14	US-10-150-475A-4

13	747	66.0	213	16	US-10-704-522-4	Sequence 4, Appli
14	747	66.0	213	16	US-10-645-215-4	Sequence 4, Appli
15	742	65.5	215	15	US-10-307-724-122	Sequence 122, App
16	742	65.5	215	16	US-10-737-290-122	Sequence 122, App
17	742	65.5	239	16	US-10-737-290-142	Sequence 142, App
18	741	65.5	213	15	US-10-435-299-12	Sequence 12, Appl
19	740	65.4	233	14	US-10-153-382-11	Sequence 11, Appl
20	740	65.4	233	16	US-10-612-497-15	Sequence 15, Appl
21	740	65.4	233	16	US-10-612-497-67	Sequence 67, Appl
22	740	65.4	233	16	US-10-776-649-15	Sequence 15, Appl
23	740	65.4	233	16	US-10-776-649-67	Sequence 67, Appl
24	739	65.3	669	9	US-09-807-721-2	Sequence 2, Appli
25	738.5	65.2	234	15	US-10-045-674-587	Sequence 587, App
26	737	65.1	215	16	US-10-128-520-106	Sequence 106, App
27	736.5	65.1	234	15	US-10-292-088-88	Sequence 88, Appl
28	735.5	65.0	214	15	US-10-364-953-1	Sequence 1, Appli
29	735.5	65.0	237	14	US-10-020-786-10	Sequence 10, Appl
30	735.5	65.0	667	16	US-10-764-428-7	Sequence 7, Appli
31	735.5	65.0	667	16	US-10-764-428-13	Sequence 13, Appl
32	735.5	65.0	667	16	US-10-764-428-25	Sequence 25, Appl
33	735.5	65.0	670	16	US-10-764-428-5	Sequence 5, Appli
34	735.5	65.0	670	16	US-10-764-428-9	Sequence 9, Appli
35	735.5	65.0	670	16	US-10-764-428-11	Sequence 11, Appl
36	735.5	65.0	670	16	US-10-764-428-27	Sequence 27, Appl
37	735	64.9	235	15	US-10-656-769-38	Sequence 38, Appl
38	734.5	64.9	237	9	US-09-056-160B-100	Sequence 100, App
39	734.5	64.9	237	14	US-10-234-671-100	Sequence 2, Appli
40	734.5	64.9	491	13	US-10-011-125-2	Sequence 79, Appl
41	734	64.8	236	14	US-10-235-175-79	Sequence 40, Appl
42	733	64.8	215	15	US-10-408-901-40	Sequence 48, Appl
43	733	64.8	215	15	US-10-408-901-52	Sequence 52, Appl
44	733	64.8	215	15	US-10-408-901-52	Sequence 52, Appl
45	733	64.8	215	16	US-10-128-520-129	Sequence 129, App

ALIGNMENTS

RESULT 1  
US-10-625-047-27  
; Sequence 27, Application US/10625047  
; Publication No. US20040198962A1  
; GENERAL INFORMATION:  
; APPLICANT: Meares, Claude  
; APPLICANT: Corneillie, Todd  
; TITLE OF INVENTION: The Regents of the University of California  
; FILE REFERENCE: 023070-130910US  
; CURRENT APPLICATION NUMBER: US/10/625,047  
; CURRENT FILING DATE: 2003-07-22  
; PRIOR APPLICATION NUMBER: US 10/350,555  
; PRIOR FILING DATE: 2003-01-23  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:native cloned  
; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region  
; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody  
; OTHER INFORMATION: kappa light chain constant region (TTCCL)

US-10-625-047-27  
Query Match 95.3%; Score 1079; DB 16; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.8e-83;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 RSAVVTQESALTTSPGETVTLTCSRSSIGAVTTSNYANWVQEKDHLFTGLIGTNNRPPG 60  
Db 1 RSAVVTQESALTTSPGETVTLTCSRSSIGAVTTSNYANWVQEKDHLFTGLIGTNNRPPG 60

Qy 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVF 120  
Db 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVF 120  
Qy 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180  
Db 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180  
Qy 181 STLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 181 STLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 218

## RESULT 2

US-10-625-047-28  
Query Match 95.2%; Score 1078; DB 16; Length 218;  
Best Local Similarity 95.9%; Pred. No. 2.2e-83;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Meares, Claude  
APPLICANT: Cornellie, Todd  
TITLE OF INVENTION: The Regents of the University of California  
FILE REFERENCE: Multi-Functional Antibodies  
CURRENT APPLICATION NUMBER: US/10/625,047  
CURRENT FILING DATE: 2003-07-22  
PRIOR APPLICATION NUMBER: US 10/350,555  
PRIOR FILING DATE: 2003-01-23  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:N53C cloned  
OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable  
OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin  
OTHER INFORMATION: antibody kappa light chain constant region (ITCL)  
US-10-625-047-28

Qy 1 RSADVQESALTTSGETVTLTCRSSIGAVTTSYANNVQEKPDHLFTGLIGGTNNRAGP 60  
Db 1 RSADVQESALTTSGETVTLTCRSSIGAVTTSYANNVQEKPDHLFTGLIGGTNNRAGP 60  
Qy 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVF 120  
Db 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVF 120  
Qy 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180  
Db 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180  
Qy 181 STLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 181 STLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 218

## RESULT 3

US-10-723-003-42  
Query Match 95.2%; Score 1078; DB 16; Length 218;  
Best Local Similarity 95.9%; Pred. No. 2.2e-83;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: MA, Jing  
APPLICANT: GUO, Yajun  
TITLE OF INVENTION: PREPARATION AND APPLICATION OF  
FILE REFERENCE: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS  
CURRENT APPLICATION NUMBER: US/10/723,003  
CURRENT FILING DATE: 2003-11-26

Qy 1 RSADVQESALTTSGETVTLTCRSSIGAVTTSYANNVQEKPDHLFTGLIGGTNNRAGP 60  
Db 1 RSADVQESALTTSGETVTLTCRSSIGAVTTSYANNVQEKPDHLFTGLIGGTNNRAGP 60  
Qy 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVF 120  
Db 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPSVF 120  
Qy 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180  
Db 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180  
Qy 181 STLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 181 STLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 218

US-10-723-003-42

Query Match 66.7%; Score 755.5; DB 16; Length 235;  
Best Local Similarity 70.5%; Pred. No. 5.2e-56;  
Matches 155; Conservative 16; Mismatches 42; Indels 7; Gaps 3;  
Qy 1 RSADVQESALTTSGETVTLTCRSSIGAVTTSYANNVQEKPDHLFTGLIGGTNNRAGP 60  
Db 21 RQGVLSQSPAILASGPEKVTMTCRAS---SSVSYIHWFPQKPGSSPKWIVATSLA 76  
Qy 59 PGVPARESGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGGTKLTVLSRTVAAPS 118  
Db 77 SGVPARESGSGSGTYSLSITISRVEADAATYCCQWTSNPPTFGGKLEI-KRTVAAPS 135  
Qy 119 VFIPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 178  
Db 136 VFIPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 195  
Qy 179 LSSTLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 196 LSSTLTLKADYKHKYKHYACEVTHQGLSPVTKSFNRGEC 235

## RESULT 4

US-09-995-693-1  
Sequence 1, Application US/09995693  
Patent No. US20020136721A1  
GENERAL INFORMATION:  
APPLICANT: Schwall, Ralph H.  
Tabor, Kelly H.  
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
Antagonists and Uses Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/995,693  
FILING DATE: 29-Nov. US20020136721A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/952,235  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P0938P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:



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; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1

Query Match          66.3%; Score 751; DB 9; Length 220;
Best Local Similarity 71.8%; Pred. No. 1.2e-55;
Matches 153; Conservative 14; Mismatches 42; Indels 4; Gaps 2;

QY 9 SALTTPSGETVTLTCRSSIGAVTTS---NYANWVQEKPDHFLTGLIGGNNRAGVPARF 65
Db 9 SSLTVSVEKVTVSKSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTRESGVPDF 68

QY 66 SGLSGDKAALITGAQTEDEARYFCALWYSCLVWFGGKTKLTVLSRTVAAPSVEIFPPS 125
Db 69 TCGSGGTDFTLTITTSVKADDLAVYYCQYYAYPWTFFGGTKLEI-KRTVAAPSVEIFPPS 127

QY 126 DEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 185
Db 128 DEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 187

QY 186 SKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 188 SKADYKHKVYACEVTHQGLSSPTKSFNRGEC 220

RESULT 5
US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,408
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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US-10-232-408-1

Query Match          66.3%; Score 751; DB 14; Length 220;
Best Local Similarity 71.8%; Pred. No. 1.2e-55;
Matches 153; Conservative 14; Mismatches 42; Indels 4; Gaps 2;

QY 9 SALTTPSGETVTLTCRSSIGAVTTS---NYANWVQEKPDHFLTGLIGGNNRAGVPARF 65
Db 9 SSLTVSVEKVTVSKSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTRESGVPDF 68

QY 66 SGLSGDKAALITGAQTEDEARYFCALWYSCLVWFGGKTKLTVLSRTVAAPSVEIFPPS 125
Db 69 TCGSGGTDFTLTITTSVKADDLAVYYCQYYAYPWTFFGGTKLEI-KRTVAAPSVEIFPPS 127

QY 126 DEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 185
Db 128 DEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 187

QY 186 SKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 188 SKADYKHKVYACEVTHQGLSSPTKSFNRGEC 220

RESULT 6
US-09-848-832-4
; Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848,832
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-848-832-4

Query Match          66.2%; Score 749.5; DB 10; Length 234;
Best Local Similarity 71.8%; Pred. No. 1.7e-55;
Matches 155; Conservative 13; Mismatches 43; Indels 5; Gaps 3;

QY 4 VVTOESA-LTTPSGETVTLTCRSSIGAVTTSNYANWVQEKPDHFLTGLIGGNNRAGVP 62
Db 23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQKPGQAPRLIYDTSNRATGIP 79

QY 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYSCLVWFGGKTKLTVLSRTVAAPSVEIF 122
Db 80 ARFSGSGSGTDFTLISISLEPEDFAVYYCQRFNWPWTFFGQTKVE-FKRTVAAPSVEIF 138

QY 123 PPSDEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 139 PPSDEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSYLSST 198

QY 183 LTLISKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 199 LTLISKADYKHKVYACEVTHQGLSSPTKSFNRGEC 234

RESULT 7
US-10-225-108A-4
; Sequence 4, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard

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; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-4

Query Match      66.2%; Score 749.5; DB 14; Length 234;
Best Local Similarity 71.8%; Pred. No. 1.7e-55;
Matches 155; Conservative 13; Mismatches 43; Indels 5; Gaps 3;

Qy      4 VVTQESA-LTTPSGTAVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
Db      23 VLTQSPATLSLSPGERATLACRAS---QTASRYLAWYQKPGQAPRLLIYDTSNRATGIP 79

Qy      63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLMVFGGGTKLTVLSTRTVAAPSVEIF 122
Db      80 ARFSGSGSGTDFTLTLSISLEPEDPAVYVCQQRFPNWPFTFGQGTKVE-FKRTVAAPSVEIF 138

Qy      123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 182
Db      139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 198

Qy      183 LTLSKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218
Db      199 LTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 9
US-10-150-475A-8
; Sequence 8, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 8 Light Chain SEQ ID NO: 8
US-10-150-475A-8

Query Match      66.2%; Score 749; DB 14; Length 213;
Best Local Similarity 72.2%; Pred. No. 1.7e-55;
Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

Qy      4 VVTQESA-LTTPSGTAVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
Db      3 VLTQSPATLSLSPGERATLACRAS---SSINYYIWLQKPGQAPRLLIYLTSLNLAGVP 58

Qy      63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLMVFGGGTKLTVLSTRTVAAPSVEIF 122
Db      59 ARFSGSGSGTDFTLTLSISLEPEDPAVYVCQQRFPNWPFTFGQGTKVEI-KRTVAAPSVEIF 117

Qy      123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 182
Db      118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSSTYSLSST 177

Qy      183 LTLSKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218
Db      178 LTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 10
US-10-704-522-8
; Sequence 8, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; QUERY MATCH: 66.2%; Score 749.5; DB 15; Length 234;
; BEST LOCAL SIMILARITY: 71.8%; Pred. No. 1.7e-55;
; MATCHES: 155; Conservative 13; Mismatches 43; Indels 5; Gaps 3;

Qy      4 VVTQESA-LTTPSGTAVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-704-522-4

Query Match      66.0%; Score 747; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.4e-55;
Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;

Qy 4 VVQESA-LTTPSGETVLTTCRSSIGAVTTSNYANWQEKDPDHLFTGLIGTNNRAPGVP 62
Db 3 VLTQSPATLSLSPGERATLSCAS-----SSNIYYWQQKPGQAPRLLIYLTSLNLSGVP 58

Qy 63 ARFSGSLGDKAALITIGTAQTEDEARYFCALWYSCLVWFGGTKLTLSRTVAAPSVFIF 122
Db 59 ARFSGSGGTDFTLTITISLEPEDFAVYVCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 177

Qy 183 LTLSKADYEHKHKYACEVTHQGLSPVTKSFNRGEC 218
Db 178 LTLSKADYEHKHKYACEVTHQGLSPVTKSFNRGEC 213

RESULT 14
US-10-645-215-4
; Sequence 4, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunocjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-645-215-4

Query Match      66.0%; Score 747; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.4e-55;
Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;

Qy 4 VVQESA-LTTPSGETVLTTCRSSIGAVTTSNYANWQEKDPDHLFTGLIGTNNRAPGVP 62
Db 3 VLTQSPATLSLSPGERATLSCAS-----SSNIYYWQQKPGQAPRLLIYLTSLNLSGVP 58

Qy 63 ARFSGSLGDKAALITIGTAQTEDEARYFCALWYSCLVWFGGTKLTLSRTVAAPSVFIF 122
Db 59 ARFSGSGGTDFTLTITISLEPEDFAVYVCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF 117

Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 177
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Qy 183 LTLSKADYEHKHKYACEVTHQGLSPVTKSFNRGEC 218
Db 178 LTLSKADYEHKHKYACEVTHQGLSPVTKSFNRGEC 213

RESULT 15
US-10-307-724-122
; Sequence 122, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2cip
; CURRENT APPLICATION NUMBER: US/10307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 215
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain
US-10-307-724-122

Query Match      65.5%; Score 742; DB 15; Length 215;
Best Local Similarity 70.8%; Pred. No. 6.6e-55;
Matches 153; Conservative 16; Mismatches 43; Indels 4; Gaps 3;

Qy 4 VVTOE-SALTTPSGETVLTTCRSSIGAVTTSNYANWQEKDPDHLFTGLIGTNNRAPGVP 62
Db 3 VLTQSPGTLSLSPGERATLSCAS--QSVSSSYLAWYQKPGQAPRLLIYGASSRATGIP 60

Qy 63 ARFSGSLGDKAALITIGTAQTEDEARYFCALWYSCLVWFGGTKLTLSRTVAAPSVFIF 122
Db 61 DRFSGSGGTDFTLTITISLEPEDFAVYVCOQYGGSPMTFGGTKVEI-KRTVAAPSVFIF 119

Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 182
Db 120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 179

Qy 183 LTLSKADYEHKHKYACEVTHQGLSPVTKSFNRGEC 218
Db 180 LTLSKADYEHKHKYACEVTHQGLSPVTKSFNRGEC 215
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Search completed: June 7, 2005, 16:18:38  
Job time : 102 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 15:39:10 ; Search time 25 Seconds  
(without alignment)  
839.010 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
Sequence: 1 RAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	740	65.4	215	2 JE0242	Ig kappa chain NIG
2	729	64.4	215	2 JE0244	Ig kappa chain NIG
3	724.5	64.0	214	2 PC4156	Ig lambda chain V
4	716	63.3	215	2 JE0243	Ig kappa chain NIG
5	692.5	60.3	216	2 JE0241	Ig kappa chain Am3
6	675	59.6	215	2 A23746	Ig kappa chain V-I
7	578.5	51.1	135	2 S52059	JC-kappa protein -
8	552.5	48.8	240	2 S06084	Ig kappa chain pre
9	544	48.1	106	1 K3HU	Ig kappa chain C r
10	543.5	48.0	287	4 PC4402	pe1B leader/Ig hea
11	537	47.4	128	2 S52450	Ig lambda chain V
12	530.5	46.9	220	2 A31790	Ig kappa chain V r
13	529	46.7	129	1 LIMS4E	Ig lambda-1 chain
14	522	46.1	235	2 S25058	Ig kappa chain - m
15	521	46.0	113	2 S06819	Ig lambda chain V
16	519.5	45.9	112	2 S06818	Ig lambda chain V
17	517	45.7	106	2 S20654	Ig kappa chain - m
18	515	45.5	219	2 S38855	Ig kappa chain - m
19	514	45.4	225	2 S37484	Ig kappa chain - m
20	509.5	45.0	114	2 S06820	Ig lambda chain V
21	509.5	45.0	234	2 S14237	Ig kappa chain pre
22	509	45.0	99	2 A37927	Ig kappa chain C r
23	506.5	44.7	230	2 S33161	Ig kappa chain - s
24	503.5	44.5	218	2 S68241	Ig kappa chain C r
25	503	44.4	99	2 S26653	Ig kappa chain C r
26	501.5	44.3	214	2 S68212	Ig kappa chain (Ma
27	499.5	44.1	225	2 JLU0029	Ig kappa chain pre
28	498.5	44.0	218	2 JC5810	monoclonal antibod
29	497.5	43.9	234	2 S01320	Ig kappa chain pre

RESULT 1  
JE0242  
Ig kappa chain NIG26 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C;Accession: JE0242  
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takaashi, I.; Shinoda, submitted to JIPID, November 1998  
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: MU  
A;Reference number: JE0241  
A;Accession: JE0242  
A;Molecule type: protein  
A;Residues: 1-215 <ALI>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-91/Domain: immunoglobulin homology <IMM>  
Query Match 65.4%; Score 740; DB 2; Length 215;  
Best Local Similarity 70.4%; Pred. No. 7.9e-49;  
Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;  
Qy 4 VTQESALTTSPGETVTLCRSSIGAVTTSYANVVOEKPDHLFTGLIGTNNRAGVP 62  
Db 3 VLTQSPGTLSPGSRATLSCRAS--QSVSNNYLAWYQKPGQAPSLLIYDASSRATGIP 60  
Qy 63 ARPSGLIGDKAALTITGAQTEDEARYFCALWVFGGKTLVLSSTVAAPSVFIF 122  
Db 61 DRFSGSGSGTDFLTITSGLEPEDFAVYCOQYDRPPWTFGQGVKVEI-KRTVAAPSVFIF 119  
Qy 123 PPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSST 182  
Db 120 PPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSST 179  
Qy 183 LTLSKADYKHKYVACEVTHQGLSXPVTKSFNRGEC 218  
Db 180 LTLSKADYKHKYVACEVTHQGLSXPVTKSFNRGEC 215

ALIGNMENTS

RESULT 2  
JE0244  
Ig kappa chain NIG2 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C;Accession: JE0244  
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; submitted to JIPID, November 1998  
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL  
A;Reference number: JE0243  
A;Accession: JE0244  
A;Molecule type: protein  
A;Residues: 1-215 <ALI>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>



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A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match      48.8%; Score 552.5; DB 2; Length 240;
Best Local Similarity 53.4%; Pred. No. 1.2e-34;
Matches 117; Conservative 24; Mismatches 73; Indels 5; Gaps 3;

Qy          4   VVTOE-SALTTSPGETVLTICRSS---IGAVTTSYANNVQEXPDHLFTGLIGTNNRAP 59
Db          23   VMTOQPSSLAVSAGETVTINCKSSQLFYSGNQKNYLAWYQQKPGOSPCLLIYWASTRQS 82
Qy          60   GVPARFGSLTGDKAAITIGAOTDEARYFCALWTSCLVWFGGTKLTVLSRTVAAPSV 119
Db          83   GVPRFRFIGSGSGTDFTLTISVVQAEDLATIYCIIQYYETPTFGAGTKLE-LKRADAAPT 141
Qy          120  FIPPSDBOLKGGTASVCLLNFPREAKVOWKVNDNALQSGNSQESVTEQDSKDSTSYSL 179
Db          142  SIFPPSTEQLATGASVCLLMNFPRDISVKWKIDGTERRDGVLDSDVDSDSDSTYSM 201
Qy          180  SSTLTLSKADYEKKHYACEVTHOGLSXPVTKSFNRGEC 218
Db          202  SSTLTLSKADYESHNLYTCVVHKTSSSPWKSFNNEC 240
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RESULT 9  
K3HU  
Ig kappa chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1980 #sequence revision 02-Jul-1998 #text change 09-Jul-2004  
C:Accession: B30562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02  
R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.  
Biochemistry 9, 3155-3161, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequen  
A:Reference number: A90562; MUID:71064023; PMID:5489770  
A:Contents: myeloma protein Eu  
A:Accession: B30562  
A:Molecule type: protein  
A:Residues: 1-106 <GOT>  
A:Cross-references: UNIPROT:P01834

A>Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
F;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; Eu, disulfide bonds  
F;Suter, L.; Bartnikol, H.U.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
A>Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ. Su  
A;Reference number: A91651; MUID:72188439; PMID:5027703  
A;Contents: Bence Jones protein Ti

A. Molecule type: protein  
A. Residues: 1-106<SUM>  
R.Hietter, P.A., Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.

A,Reference number: A90806; MUID:81042304; PMID:6775818  
A,Accession: A90806  
A,Molecule type: DNA  
A,Residues: 1-106 <HIE>  
A,Cross-references: GB:J00241; NID:G33140; PIDN:CRAA23823.1; PID:gl335148  
A,Note: the sequence was determined from the germline gene  
R.Hiltschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,  
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,  
A,Reference number: A94417  
A,Contents: Bence Jones protein Roy  
A,Accession: A94417

A:Molecule type: protein  
A:Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HI>  
A>Note: This sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu  
R:Hilsechmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
A:Title: Die Aminosäuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).  
A:Reference number: A91639; MUID:68242259; PMID:5586923  
A:Contents: Bence Jones protein Cum  
A:Accession: A91639  
A:Molecule type: protein  
A:Residues: 1-56, 'Q', 58-106 <HI2>  
J:Titani, K.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete  
A:Reference number: A92047; MUID:69234734; PMID:4893682  
A:Contents: Bence Jones protein Ag  
A:Accession: A92047  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <TI>  
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 56-59, 1970  
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.  
A:Reference number: A94242; MUID:70201507; PMID:5447531  
A:Contents: Waldenstrom's macroglobulin Ou  
A:Accession: A94242  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <KOH>  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A>Note: allotype Inv(3)  
R:Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
A:Contents: annotation  
C:Genetics:  
A:Gene: GDB:IGKC  
A:Cross-references: GDB:120088; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds; in some cases, such as IgA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental  
Query Match 48.1%; Score 544; DB 1; Length 106;  
Best Local Similarity 99.1%; Pred. No. 2.2e-34;  
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 113 TVAAPSVFPPSPDQLSGTASVVCLNNFYPRKAVQWVDNALQSGNSQESVTEQDS 172  
Db 1 TVAAPSVFPPSPDQLSGTASVVCLNNFYPRKAVQWVDNALQSGNSQESVTEQDS 60  
Qy 173 KDSTVSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSNRGEC 218  
Db 61 KDSTVSLSTLTLSKADYKHKVYACEVTHQGLSPVTKSNRGEC 106  
RESULT 10  
PC4402  
peB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -  
C:Species: synthetic  
C:Date: 06-Nov-1998 #sequence\_revision 06-Nov-1998 #text\_change 06-Nov-1998  
C:Accession: PC4402  
R:Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.

J. Biochem. 122, 322-329, 1997  
A:Title: Construction, bacterial expression, and characterization of hapten-specific sin  
A:Reference number: PC4402  
A:Accession: PC4402  
A:Molecule type: DNA  
A:Residues: 1-287 <SUZ>  
C:Keywords: fusion protein  
Query Match 48.0%; Score 543.5; DB 4; Length 287;  
Best Local Similarity 53.4%; Pred. No. 6.9e-34;  
Matches 126; Conservative 14; Mismatches 49; Indels 47; Gaps 6;  
Qy 3 AVTQESALTTSPGETVTLTCRSSIGAVTTSNANWVQEKPDHLFTGLIGTNNRAPGVP 62  
Db 27 AVTQESALTTSPGETVTLTCRSSIGAVTTSNANWVQEKPDHLFTGLIGTNNRAPGVP 86  
Qy 63 ARFSGSLIGDKAALITITGAQTEDEARYFCALWYSCLVVFGGTTKLTVLSTVAAP----- 117  
Db 87 ARFSGSLIGDKAALITITGAQTEDEARYFCALWYSCLVVFGGTTKLTVLSSADDAKDDAK 146  
Qy 118 -----SVFPPSPDQLKSG-TASVVCLNNFYPRKAVQW----- 152  
Db 147 KDDAKDDAKDQGVOLQOPGAELVKGASVYKLSCKASGYTFTSYMHWKQRPGRGLEW 206  
Qy 153 --KVDNALQSG-----NSQSVTEQDSKDSYSLSTLTLSKADYKHKVYAC 198  
Db 207 IGRIDP--NSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLT-----SEDSAVYYC 255  
RESULT 11  
S52450  
Ig lambda chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S52450  
R:Berdoz, J.; Kraehenbuhl, J.P.  
submitted to the EMBL Data Library, November 1994  
A:Description: Specific amplification by the polymerase chain reaction of rearranged ge  
A:Reference number: S52445  
A:Accession: S52450  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-128 <BER>  
A:Cross-references: EMBL:X82687; NID:g673448; PIDN:CAA58008.1; PID:g673449  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-111/Domain: immunoglobulin homology <IMM>  
Query Match 47.4%; Score 537; DB 2; Length 128;  
Best Local Similarity 96.3%; Pred. No. 9.1e-34;  
Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 AVTQESALTTSPGETVTLTCRSSIGAVTTSNANWVQEKPDHLFTGLIGTNNRAPGVP 62  
Db 21 AVTQESALTTSPGETVTLTCRSSIGAVTTSNANWVQEKPDHLFTGLIGTNNRAPGVP 80  
Qy 63 ARFSGSLIGDKAALITITGAQTEDEARYFCALWYSCLVVFGGTTKLTVL 110  
Db 81 ARFSGSLIGDKAALITITGAQTEDEARYFCALWYSCLVVFGGTTKLTVL 128  
RESULT 12  
A31790  
Ig kappa chain V region (17/9) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C:Accession: A31790  
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an an  
A:Reference number: A92686; MUID:89034213; PMID:3182835



A:Accession: A31790  
A:Molecule type: mRNA  
A:Residues: 1-220 <SCH>  
A:Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 530.5; DB 2; Length 220;  
Best Local Similarity 51.6%; Pred. No. 5e-33;  
Matches 113; Conservative 26; Mismatches 75; Indels 5; Gaps 3;

QY 4 VVTQESALTTSPGFTVTLTCRSS---IGAVTTSYANVWQKPDHFLFTGLIGGTNNRAP 59  
DB 3 VMTQSPSSLTVTAGEKVTWMSCTSSQSLFNSGKQKNTLTWTYQKPGQPPKVLIIWASTRES 62

QY 60 GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCILWVFGGTPKLVLSRTVAAPSV 119  
DB 63 GVPDRFTGSGSGTDFLTITSSVQAEADLVYQNDYSNPLTFTGGGTPKLE-LKRADAAPTV 121

QY 120 FIPPSDEQLKSTASVCLLNFPYREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 179  
DB 122 SIFPPSSEQLTSGCAGVGVCFVNNFYPKDINVKWIDGSRQNGVLNSWTDQDSKSTYSM 181

QY 180 SSTLTSLKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218  
DB 182 SSTLTTLTKDEYHRHNSYTCEATHKSTSTSFIVKSFNRNEC 220

RESULT 13  
LIMS4E  
Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43)  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Sep-1981 #sequence\_revision 24-Sep-1981 #text\_change 09-Jul-2004  
C:Accession: B93815; B93775; C93784; B93784; A90780; C93282; A01995  
R:Burstein, Y.; Schechter, I.  
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977  
A:Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors  
A:Reference number: A93815; MUID:77148916; PMID:403522  
A:Contents: MOPC 104E  
A:Accession: B93815  
A:Molecule type: protein  
A:Residues: 1-29 <BUR>  
A:Cross-references: UNIPROT:P01724  
A:Note: this precursor was synthesized in a cell-free system directed by messenger RNA in d after synthesis  
R:Appella, E.  
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971  
A:Title: Amino acid sequences of two mouse immunoglobulin lambda chains.  
A:Reference number: A93775; MUID:71107854; PMID:5276767  
A:Contents: MOPC 104E; RPC 20  
A:Accession: B93775  
A:Molecule type: protein  
A:Residues: '2', 21-25, 'Q', 27-129 <APP>  
A:Accession: C93775  
A:Molecule type: protein  
A:Residues: 20-129 <AP2>  
A:Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E  
R:Cesari, I.M.; Weigert, M.  
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973  
A:Title: Mouse lambda-chain sequences  
A:Reference number: A93784; MUID:73229669; PMID:4516208  
A:Contents: J558; S104; S178  
A:Accession: A93784  
A:Molecule type: protein  
A:Residues: 20-129 <CES>  
A:Accession: B93784  
A:Molecule type: protein  
A:Residues: 20-129 <CE2>  
A:Accession: C93784  
A:Molecule type: protein  
A:Residues: 20-43, 'N', 45-70, 'N', 72-115, 'R', 117-129 <CE3>  
A:Note: these proteins were isolated from serum or urine of tumor-bearing mice

R:Bernard, O.; Hozumi, N.; Tonegawa, S.  
Cell 15, 1133-1144, 1978  
A:Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch  
A:Reference number: A90780; MUID:79084170; PMID:103630  
A:Contents: H2020  
A:Accession: A90780  
A:Molecule type: DNA  
A:Residues: 1-43, 'T', 45-50, 'G', 52-58, 'E', 60-89, 'D', 91-129 <BER>  
A:Note: the sequence was determined from the differentiated gene  
R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Inanishi-Kari, T.; Rajewsky, K.; Baltimore, I  
Nature 298, 380-382, 1982  
A:Title: Somatic variants of murine immunoglobulin lambda light chains.  
A:Reference number: A93282; MUID:82220143; PMID:6283385  
A:Contents: S43  
A:Accession: C93282  
A:Molecule type: DNA  
A:Residues: 1-58, 'E', 60-89, 'D', 91-98, 'T', 100-105, 'M', 107-129 <BOT>  
A:Note: the sequence was determined from the differentiated gene  
C:Comment: The MOPC 104E sequence is shown.  
C:Genetics:  
A:Introns: 16/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; pyroglutamic acid  
F:1-19/Domain: signal sequence #status experimental <SIG>  
F:20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>  
F:34-111/Domain: immunoglobulin homology <IMM>  
F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime  
F:41-109/Disulfide bonds: #status predicted

Query Match 46.7%; Score 529; DB 1; Length 129;  
Best Local Similarity 94.4%; Pred. No. 3.7e-33;  
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 AVVTQESALTTSPGFTVTLTCRSSIGAVTTSYANVWQKPDHFLFTGLIGGTNNRAPGVP 62  
DB 21 AVVTQESALTTSPGFTVTLTCRSSIGAVTTSYANVWQKPDHFLFTGLIGGTNNRAPGVP 80

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCILWVFGGTPKLV 110  
DB 81 ARFSGSLIGNKAALTITGAQTEDEARYFCALWYSCILWVFGGTPKLV 128

RESULT 14  
S25058  
Ig kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S25058  
R:Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific  
A:Reference number: S25057  
A:Accession: S25058  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-235 <FIS>  
A:Cross-references: EMBL:X67211; NID:G54828; PIDN:CAA47650.1; PID:G54829  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 46.1%; Score 522; DB 2; Length 235;  
Best Local Similarity 50.5%; Pred. No. 2.3e-32;  
Matches 109; Conservative 29; Mismatches 72; Indels 6; Gaps 3;

QY 4 VVTQESA-LTTSFGFTVTLTCRSSIGAVTTSYANVWQKPDHFLFTGLIGGTNNRAPGVP 62  
DB 25 VLTQSPALMSASPGKVTWTCSSAS---SSVSKQWVYQKSGTSPKRWIYDTSKLASGVP 80

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCILWVFGGTPKLV 122  
DB 81 GRFSGSGTGYSLTITSSMEAEADATYVCOQSSNPLTFGAGTKLE-LKRADAAPTYSIF 139

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QY 123 PPSBQLKSGTASVVCLLNFPYBPAKQVQKVDNALQSGNQSVTEQDSKDSYSLSSST 182
Db 140 PPSBQLTSGGASVVCFLNFPYKIDINVKWKIDGSEKQGVNLNSWTQDSKDSYSSMSST 199
QY 183 LTLSKADYEKHKVACEVTHOGLSXPTKSFNRGEC 218
Db 200 LTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235

RESULT 15
S06819
Ig lambda chain V region (clone 10C3) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C:Accession: S06819
R:Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A:Reference number: S06815; MUID:90064531; PMID:2555519
A:Accession: S06819
A:Molecule type: mRNA
A:Residues: 1-113 <MIL>
A:Cross-references: EMBL:X17168; NID:952251; PIDN:CAA35046.1; PID:9930172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-91/Domain: immunoglobulin homology <IMM>
F:21-89/Disulfide bonds: #status predicted

Query Match 46.0%; Score 521; DB 2; Length 113;
Best Local Similarity 94.4%; Pred No. 1,3e-32;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWQEKPDHLFTGLIGTNNRAPGVP 62
Db 1 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWQEKPDHLFTGLIGTNNRAPGVP 60

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSLWVFGGGTKLTVL 110
Db 61 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSLWVFGGGTKLTVL 108
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Search completed: June 7, 2005, 16:01:07  
Job time : 26 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:37:31 ; Search time 111 Seconds  
(without alignments)  
1005.705 Million cell updates/sec

Title: US-09-671-953B-5  
Perfect score: 1132  
Sequence: 1 R5AVVQESALTTSPGETVT.....EVTHQGLSPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734	64.8	235	Q6PJF2	Q6pjf2 homo sapien
2	733	64.8	235	Q6GMW0	Q6gmw0 homo sapien
3	732	64.7	236	Q6GMW1	Q6gmw1 homo sapien
4	727.5	64.3	236	Q7Z3Y4	Q7z3y4 homo sapien
5	727	64.2	234	Q7Z473	Q7z473 homo sapien
6	723.5	63.9	236	Q6PIH7	Q6pih7 homo sapien
7	722.5	63.8	236	Q6GMX9	Q6gmx9 homo sapien
8	721.5	63.7	236	Q6P5S8	Q6p5s8 homo sapien
9	721	63.7	235	Q6GMV9	Q6gmv9 homo sapien
10	720.5	63.6	236	Q6GMX0	Q6gmx0 homo sapien
11	717.5	63.4	236	Q6PIL8	Q6pil8 homo sapien
12	715.5	63.2	236	Q6GMX8	Q6gmx8 homo sapien
13	704	62.2	236	Q6PIT5	Q6pit5 homo sapien
14	702.5	62.1	236	Q6PIH4	Q6pih4 homo sapien
15	697	61.6	239	Q8TCD0	Q8tcd0 homo sapien
16	696	61.5	240	Q6PIH6	Q6pih6 homo sapien
17	694	61.3	239	Q8NEK0	Q8nek0 homo sapien
18	666	58.8	239	Q6P491	Q6p491 homo sapien
19	564.5	49.9	120	Q6P5R5	Q6p5r5 homo sapien
20	544	48.1	106	KAC HUMAN	P01834 homo sapien
21	535	47.3	129	LV1E MOUSE	P01727 mus musculus
22	530	46.8	129	LV1D MOUSE	P01726 mus musculus
23	529	46.7	129	LV1B MOUSE	P01724 mus musculus
24	523	46.2	129	Q8VDE2	Q8vde2 mus musculus
25	522.5	46.2	238	Q6GJS7	Q6gjs7 mus musculus
26	521	46.0	110	LV1C MOUSE	P01725 mus musculus
27	514.5	45.5	113	Q8CGS1	Q8cgs1 mus musculus
28	510.5	45.1	236	Q7TS98	Q7ts98 mus musculus
29	507.5	44.8	109	Q9ET13	Q9et13 mus musculus
30	502	44.3	219	Q65ZC0	Q65zc0 mus musculus
31	497.5	43.9	241	Q63ZX4	Q63zx4 mus musculus

32 491 43.4 129 1 LV2B MOUSE P01729 mus musculus  
33 477 42.1 117 1 LV1A\_MOUSE P01723 mus musculus  
34 454 40.1 117 1 LV2A\_MOUSE P01728 mus musculus  
35 442.5 39.1 236 2 Q8NEJ1 Q8nej1 homo sapien  
36 440 38.9 235 2 Q6IN99 Q6in99 homo sapien  
37 435 38.4 248 2 Q7SYU1 Q7syu1 xenopus lae  
38 432 38.2 233 2 Q8TBC9 Q8tbc9 homo sapien  
39 430.5 38.0 230 2 Q7Z2U3 Q7z2u3 homo sapien  
40 430.5 38.0 236 2 Q6PIQ7 Q6piq7 homo sapien  
41 428.5 37.9 236 2 Q6GMV7 Q6gmv7 homo sapien  
42 428.5 37.9 236 2 Q6IPQ0 Q6ipq0 homo sapien  
43 427.5 37.8 234 2 Q7Z2U7 Q7z2u7 homo sapien  
44 426.5 37.7 236 2 Q6GMX4 Q6gmx4 homo sapien  
45 426 37.6 231 2 Q6GNB8 Q6gnb8 xenopus lae

RESULT 1  
Q6PJF2 PRELIMINARY; PRT; 235 AA.  
AC Q6PJF2;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein.  
DE OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywicki M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) .

ALIGNMENTS

DR SMART: SM00409; IG: 2.  
DR SMART: SM00407; IGC1; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein\_  
SQ SEQUENCE 235 AA; 25765 MW; 4360C36BD4133F5 CRC64;

Query Match 64.8%; Score 733; DB 2; Length 235;  
Best Local Similarity 70.5%; Pred. No. 1.9e-56;  
Matches 153; Conservative 17; Mismatches 41; Indels 6; Gaps 4;

Qy 4 VVTOESA-LTTPSGETVTLTCSRSSIGAVTTSYANVWQKPDHLFTGLIGTNNRAPGVP 62  
Db 23 VLTQSPATLSLSPGERATLSCRAS--QIVSSAYLAWYQKQPGQAPRLLMFGSSSRATGIP 80  
Qy 63 ARESGSLIGDKAALTTGAQTEDEARYFCALMYSCILWVFGGKTKLTVLSRTVAAPSVEIF 122  
Db 81 DRESGSGSGTDFLTISRLEPEDFAVYCCQYQSGGTGPGTKVDI-KRTVAAPSVEIF 139  
Qy 123 PPDEOLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182  
Db 140 PPDEOLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 199  
Qy 183 LTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 218  
Db 200 LTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 235

RESULT 2  
Q6GMW0 ID Q6GMW0 PRELIMINARY; PRT; 235 AA.  
AC Q6GMW0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Uddin T.B., Toshlyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RX [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073792; AAH73792.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; Ig; 2.

DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig cl.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; IG1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25751 MW; 5BPE6A087AFAC437 CRC64;

Query Match 64.7%; Score 732; DB 2; Length 236;  
Best Local Similarity 70.0%; Pred. No. 2.3e-56;  
Matches 154; Conservative 16; Mismatches 44; Indels 6; Gaps 4;

QY 1 RSAA-VTQE-SALTTPGGETVTLTCRSSIGAVTTSNYANNVQEKPDHFLTGLIGTNNRA 58  
DB 21 RCAIQWTFSSLSASVGRVITTCRASQ---ISNDLGYQKPKAPKLLIYAASSIQ 77  
QY 59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGKTKLTVLSRTVAAPS 118  
DB 78 SGVPSRFSGSGGTDFTLTISLQPEDFATYYCQYKSPVTFQGTQKVEI-KRTVAAPS 136  
QY 119 VFIPPSDQLSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYTS 178  
DB 137 VFIPPSDQLSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYTS 196  
QY 179 LASTLTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
DB 197 LSTLTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 236

RESULT 4  
Q723Y4 PRELIMINARY; PRT; 236 AA.  
ID Q723Y4  
AC Q723Y4  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;

RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBAJ databases.  
DR EMBL; BC005332; AAH05332.1; -.  
DR HSSP; P01834; IHEZ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25702 MW; 7BFE4ED23084BC6 CRC64;

Query Match 64.3%; Score 727.5; DB 2; Length 236;  
Best Local Similarity 70.7%; Pred. No. 5.7e-56;  
Matches 152; Conservative 15; Mismatches 43; Indels 5; Gaps 3;

QY 5 VTOE-SALTTPGGETVTLTCRSSIGAVTTSNYANNVQEKPDHFLTGLIGTNNRAPGVA 63  
DB 26 WTQSPSSLSASVGRVITTCRAS---QDISNLANFWQKPKAPKSLIYGASSLQSGVQS 82  
QY 64 RFGSLIGDKAALTITGAQTEDEARYFCALWYSCLVWFGGKTKLTVLSRTVAAPSVFIPP 123  
DB 83 RFGSGSGGTDFTLTISLQPEDFATYYCQYKSPVTFQGTQKVEI-KRTVAAPSVFIPP 141  
QY 124 PSDEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYTSLSSTL 183  
DB 142 PSDEQLKSGTASVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDYTSLSSTL 201  
QY 184 TLSKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
DB 202 TLSKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 236

RESULT 5  
Q72473 PRELIMINARY; PRT; 234 AA.  
ID Q72473  
AC Q72473  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]

RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung;
RA	Strausberg R.,
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBDJ databases.
DR	EMBL; BC034141; AAH34141.1; -,
DR	HSP; P01607; IAR2.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig.cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig.v.
DR	Pfam; PF07654; C1-set; 1.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGC1; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS00835; IG_LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Hyposethical protein.
KW	Proteoretical protein.
QY	SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
QY	Query Match 63.9%; Score 723.5; DB 2; Length 236;
DB	Best Local Similarity 70.7%; Pred. No. 1.3e-55;
DB	Matches 152; Conservative 14; Mismatches 44; Indels 5; Gaps 3;
QY	5 VTQE-SALTSPQETVTLTCRSSIGAVTTSNVAWVQEKPDHLFTGLIGGTNNRAPGVPA 63
DB	26 LTQSPFLGASVGRVTTTCRASQG---ISSYLVWYQQKPKAPNLLIYAASTLQSGVPS 82
QY	64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGTKLTVLSRTVAAPSVFIPP 123
DB	83 RFSSGSGTEFTLTISLQPEDFATVYCCQLNSSPPTFGGTVKEI-KRTVAAPSVFIPP 141
QY	124 PSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTTQDSKDSYLSLSTL 183
DB	142 PSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTTQDSKDSYLSLSTL 201
QY	184 TLSKADYERHKVYACEVTHQGLSPVTKSFNKGEC 218
DB	202 TLSKADYERHKVYACEVTHQGLSPVTKSFNKGEC 236
RESULT 7	
Q6GMX9	PRELIMINARY; PRT; 236 AA.
ID	Q6GMX9
AC	Q6GMX9
DT	05-JUL-2004 (T-EMBLrel. 27, Created)
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Primary B-Cells;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marudan K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Boak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA · Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RA "generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2].  
RN SEQUENCE FROM N.A.  
RP TISSUE=Glandular pool- thyroid;  
RC Strauberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC062704; AAH62704.1; -;  
DR HSSP; P01837; 1KCU.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25773 MW; 953E37BBB4FF5F27 CRC64;

Query Match 63.7%; Score 721.5; DB 2; Length 236;  
Best Local Similarity 70.0%; Pred. No. 1.9e-55;  
Matches 152; Conservative 16; Mismatches 44; Indels 5; Gaps 4

Qy 4 VTQGE-SALTTSQGETVTLTCRSSIGAVTTSNYANWQEKPDHLPTGLIGGTNNRAPGVP 62  
Db 23 VLTQSGPTLSFSPGERATLSCRAS--QTVFSSHLAWYQORFGQAPRLLIYGNSRATGIP 80  
Qy 63 ARFSGSLIGDKAALTIITGAOTDEARYFCALW-YSLWVFGGTKLTVLSRTVAAPSVP 121  
Db 81 DRFSGSGGTDFTLTITRLEPEDFAVFCQYGTSPSLTFGGGTRVEI-KRTVAAPSVP 139  
Qy 122 FPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKNALQSGNSQESVTEQDSKDYSLSS 181  
Db 140 FPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKNALQSGNSQESVTEQDSKDYSLSS 199  
Qy 182 TLTLISKADYEKHVYACEVTHOGLSXPVTKSFNRGEC 218  
Db 200 TLTLISKADYEKHVYACEVTHOGLSXPVTKSFNRGEC 236

RESULT 9  
Q6GMV9 PRELIMINARY; PRT; 235 AA.  
ID Q6GMV9;  
AC Q6GMV9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID:9606;  
RN [1].  
RN SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

```

RA Diatchenko L., Soares M.B., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownsrein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073793; AAH73793.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 63.7%; Score 721; DB 2; Length 235;
Best Local Similarity 69.4%; Pred. No. 2.1e-55;
Matches 150; Conservative 15; Mismatches 45; Indels 4; Gaps 3;

Qy 4 VVTQF-SALTTSPGETVTLTCRSSIGAVTTSNYANWQEKPDHLFTGLIGTNNRAPGVP 62
Db 23 VLTQSPGTLISLSPGERALSCRA--QSVNSKYLAWYQKQKQAPRLMLYASIRATGIP 80

Qy 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYSCLVWVFGGKTLVLSRTVAAPSVFIF 122
Db 81 DRFGSGSGTDPTLTISRLESEDFALYFCQYQYGTSPITFGGKTKVEI-KRTVAAPSVFIF 139

Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 199

Qy 183 LTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
Db 200 LTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 235

RESULT 10
Q6GMX0 PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;

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RX MEDLINE=22389257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073793; AAH73793.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 63.6%; Score 720.5; DB 2; Length 236;
Best Local Similarity 69.3%; Pred. No. 2.4e-55;
Matches 149; Conservative 17; Mismatches 44; Indels 5; Gaps 3;

Qy 5 VVTQF-SALTTSPGETVTLTCRSSIGAVTTSNYANWQEKPDHLFTGLIGTNNRAPGVP 63
Db 26 MTQSPSSLSASVGRVTITCRAS--QNINNYLNWYQLKPGKAPNLLIYAASSLSQGVPS 82

Qy 64 RFGSGLIGDKAALITGAQTEDEARYFCALWYSCLVWVFGGKTLVLSRTVAAPSVFIF 123
Db 83 RFGSGSGTDPTLTISRLESEDFALYFCQYQYGTSPITFGGKTKVEI-KRTVAAPSVFIF 141

Qy 124 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTL 183
Db 142 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTL 201

Qy 184 TLTKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
Db 202 TLTKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 236

RESULT 11
Q6PIL8 PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC024511; AA32451.1; -  
DR HSSP; P01837; 1KCU.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00407; IGC1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;  
Query Match 63.4%; Score 717.5; DB 2; Length 236;  
Best Local Similarity 69.6%; Pred. No. 4.4e-55;  
Matches 151; Conservative 18; Mismatches 43; Indels 5; Gaps 4;  
QY 4 VVTQE-SALITSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62  
Db 23 VLTQSPCTLSLSPGERATLSCRAS-QSLSSSYLAWYQKPGQAPRLIYGVSSRATGIP 80  
QY 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYSCLWV-FGGTKLTVLSRTVAAPSFI 121  
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCYQYGTSTRFTFGQGLDI-KRTVAAPSFI 139  
QY 122 FPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSS 181  
Db 140 FPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSS 199  
QY 182 TLTLKADYKHKYACEVTHQGLSPVTKSFNRGEC 218  
Db 200 TLTLKADYKHKYACEVTHQGLSPVTKSFNRGEC 236  
RESULT 12  
Q6GMX8 PRELIMINARY; PRT; 236 AA.  
ID Q6GMX8  
AC Q6GMX8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073764; AAH73764.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00407; IGC1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
Query Match 63.2%; Score 715.5; DB 2; Length 236;  
Best Local Similarity 69.3%; Pred. No. 6.6e-55;  
Matches 149; Conservative 19; Mismatches 42; Indels 5; Gaps 3;  
QY 5 VTQE-SALITSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 63  
Db 26 MTQSPSSASVDGVITITCRASQG---ISSWLAWYQKPGKAPKLLIYAASSLQSGVPS 82  
QY 64 RFSGSLIGDKAALITGAQTEDEARYFCALWYSCLWVFGGTTKTLTVLSRTVAAPSFI 123  
Db 83 RFSGSGSGTDFTLTISRLEPEDFAVYCYQYGTSTRFTFGQGLDI-KRTVAAPSFI 141  
QY 124 PSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSS 183  
Db 142 PSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSS 201  
QY 184 TLTKADYKHKYACEVTHQGLSPVTKSFNRGEC 218  
Db 202 TLTKADYKHKYACEVTHQGLSPVTKSFNRGEC 236

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RESULT 13
Q6PITS PRELIMINARY; PRT; 236 AA.
ID Q6PITS
AC Q6PITS
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchéz A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029444; AAH29444.1; -
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;

Query Match 62.2%; Score 704; DB 2; Length 236;
Best Local Similarity 69.1%; Pred. No. 6.8e-54;
Matches 152; Conservative 15; Mismatches 47; Indels 6; Gaps 4;

Qy 1 RSAA-VTQE-SALITSPGETVTLTCRSSIGAVTTSNYANWQKPDHFLTGLIGTNNRA 58
Db 21 RCAIQLTQSPSLASVGERVITTCRASQG---ISSALAWYQKPKPKLLIYDASTME 77

Qy 59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSLWVFGGTTKLTVLRSRTVAAPS 118
Db 78 SGVPSRFRSGSGTHTITISLQPEDATFYCQOFKSYPRTFGGTTLLEI-KRTVAAPS 136

Qy 119 VFIPFPPSEQLKSGTASVCLLNPNYPREAKVQWVDNALSGNSQESVTQDSKDYTS 178
Db 137 VFIPFPPSEQLKSGTASVCLLNPNYPREAKVQWVDNALSGNSQESVTQDSKDYTS 196

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QY 124 PSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSYSLSSTL 183  
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QY 184 TLISKADYERKHVYACVETHQGLSXPTVTKSFNRGEC 218  
DB 202 TLISKADYERKHVYACVETHQGLSXPTVTKSFNRGEC 236  
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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
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RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022362; AAH22362.1; -.  
DR PIR; S22658; S22658.  
DR PIR; S34095; S34095.  
DR PIR; S40324; S40324.  
DR PIR; S40374; S40374.  
DR PIR; S42267; S42267.  
DR PIR; S42268; S42268.  
DR HSSP; P01834; 1I7Z.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 61.6%; Score 697; DB 2; Length 239;  
Best Local Similarity 67.4%; Pred. No. 2.8e-53;  
Matches 149; Conservative 15; Mismatches 47; Indels 10; Gaps 5;

QY 4 VVTQES-ALTTPSGETVTLTCRESSIGAVTT--SNVANWVQEKPDHLFTGLIGTNNRAPG 60  
DB 23 VNTQPLSLPVLTLGQPASISCKSTQSLVYSDGNTYLNWFOQRPQSPRLIYKVSNRDSG 82  
QY 61 VPAREFSGSLIGDKAAALTITGAQTDEARYFC---ALWYSLWVFGGGLKLTVLSTRTVAAP 117  
DB 83 VPDRFSGSGSGTDFTLKITRVEAEDVGVFCMQGTHWPS---TFGQGTKLEI-KRTVAAP 138  
QY 118 SVFIPTPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSY 177  
DB 139 SVFIPTPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSY 198  
QY 178 SLSSSTLTLSKADYERKHVYACVETHQGLSXPTVTKSFNRGEC 218  
DB 199 SLSSSTLTLSKADYERKHVYACVETHQGLSXPTVTKSFNRGEC 239

Search completed: June 7, 2005, 16:00:11  
Job time : 113 secs

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3	1113	98.1	218	4	AAB20358	Anti-chel	
4	1083	95.5	218	8	ADQ98050	Chimeric	
5	1082	95.4	218	8	ADQ98051	Chimeric	
6	779	68.7	215	8	ADR23362	Human C2B	
7	759.5	67.0	235	5	AAB27925	Human C2B	
8	759.5	67.0	235	6	ABE82834	Antibody	
9	759	66.9	213	2	AD192471	Antibody	
10	757	66.8	235	2	AAW82740	Plasmid p	
11	754.5	66.5	235	3	AAB08025	A dimeric	
12	753	66.4	213	6	AAE34878	BIWA4/8 a	
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14	753	66.4	213	8	ADO00853	Humanised	
15	751	66.2	213	6	AAE35326	Humanised	
16	751	66.2	213	6	AAE34877	BIWA4 ant	
17	751	66.2	213	8	ADL15441	Humanised	
18	751	66.2	213	8	ADO00849	Humanised	
19	751	66.2	236	2	ADP79579	Chimeric	
20	750	66.1	220	2	AAW07528	Anti-HGF	
21	746	65.8	215	8	ADQ31891	Antibody	
22	744	65.6	215	8	ADQ31895	Antibody	
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XX AAB20359  
XX ID AAB20359 standard; protein; 218 AA.  
XX AC AAB20359;  
XX DT 11-JUN-2001 (first entry)  
XX DE Anti-chelate antibody CHA255 light chain.  
XX KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
XX KW cancer; therapy.  
XX OS Mus musculus.  
XX FH Key  
XX FT Region 1. .23  
XX FT /label= PR1  
XX FT /note= "framework region 1"  
XX FT Region 24. .37  
XX FT /label= CDR1  
XX FT /note= "complementarity determining region 1"  
XX FT Region 38. .52  
XX FT /label= PR2  
XX FT /note= "framework region 2"  
XX FT Region 53. .59  
XX FT /label= CDR2  
XX FT /note= "complementarity determining region 2"  
XX FT Region 60. .92  
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XX FT /note= "framework region 3"  
XX FT Region 93. .100  
XX FT /label= CDR3  
XX FT /note= "complementarity determining region 3"  
XX FT Misc-difference 100  
XX FT /note= "encoded by GTR"  
XX FT Region 101. .131  
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XX FT /note= "framework region 4"  
XX FT Misc-difference 112  
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XX FT Misc-difference 113  
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XX FT Misc-difference 206  
XX FT /note= "encoded by AGY"  
XX FT Misc-difference 207  
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XX PN WO200122922-A2.  
XX PD 05-APR-2001.  
XX PF 27-SEP-2000; 2000WO-US026619.  
XX PR 27-SEP-1999; 99US-0156194P.  
XX PR 31-MAY-2000; 2000US-0208684P.  
XX PA (REGC ) UNIV CALIFORNIA.  
XX PI Meares C, Chmura A;  
XX DR WPI; 2001-244971/25.  
XX DR N-PSDB; AAF30635.  
XX PT Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly cancer.  
XX PS Disclosure; Fig 14; 100pp; English.  
XX CC The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The reactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain variable region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C mutation. As an example of the method of the invention, rational computer aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a human/mouse chimeric Fab fragment that could be expressed in Escherichia coli, and the synthesis and screening of benzyl-EDTA chelates carrying weakly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site directed mutagenesis of a nucleic acid encoding the wild-type of the anti-chelate antibody

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Best Local Similarity 100.0%; Pred. No. 3.9e-79;  
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QY 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVF 120  
DB 61 VPARESGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVF 120  
QY 121 IFPPSDEQLKSGTASVVCVLLANFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180  
DB 121 IFPPSDEQLKSGTASVVCVLLANFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180  
QY 181 STLTLKADYKHKYACEVTHQGLSXPTVTSFNRGEC 218  
DB 181 STLTLKADYKHKYACEVTHQGLSXPTVTSFNRGEC 218

RESULT 2  
AAB20359  
XX ID AAB20359 standard; protein; 218 AA.  
XX AC AAB20359;  
XX DT 11-JUN-2001 (first entry)  
XX DE Anti-chelate antibody CHA255 light chain.  
XX KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
XX KW cancer; therapy.  
XX OS Mus musculus.  
XX FH Key  
XX FT Region 1. .23  
XX FT /label= PR1  
XX FT /note= "framework region 1"  
XX FT Region 24. .37  
XX FT /label= CDR1  
XX FT /note= "complementarity determining region 1"  
XX FT Region 38. .52  
XX FT /label= PR2  
XX FT /note= "framework region 2"  
XX FT Region 53. .59  
XX FT /label= CDR2  
XX FT /note= "complementarity determining region 2"  
XX FT Region 60. .92  
XX FT /label= PR3  
XX FT /note= "framework region 3"  
XX FT Region 93. .100  
XX FT /label= CDR3  
XX FT /note= "complementarity determining region 3"  
XX FT Misc-difference 100  
XX FT /note= "encoded by GTR"  
XX FT Region 101. .131  
XX FT /label= PR4  
XX FT /note= "framework region 4"  
XX FT Misc-difference 112  
XX FT /note= "encoded by CGW"  
XX FT Misc-difference 113  
XX FT /note= "encoded by ACK"  
XX FT Misc-difference 206  
XX FT /note= "encoded by AGY"  
XX FT Misc-difference 207  
XX FT /note= "encoded by TYG"  
XX PN WO200122922-A2.  
XX PD 05-APR-2001.  
XX PF 27-SEP-2000; 2000WO-US026619.  
XX PR 27-SEP-1999; 99US-0156194P.  
XX PR 31-MAY-2000; 2000US-0208684P.  
XX PA (REGC ) UNIV CALIFORNIA.  
XX PI Meares C, Chmura A;  
XX DR WPI; 2001-244971/25.  
XX DR N-PSDB; AAF30634.  
XX PT Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly cancer.  
XX PS Disclosure; Fig 13; 100pp; English.  
XX CC The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a

CC complementarity determining region (CDR) that specifically binds to a  
CC metal chelate against which the wild-type antibody is raised. The  
CC reactive site of the mutant antibody is in a position proximate to or  
CC within the CDR, such that the chelate and the antibody are able to form a  
CC covalent bond. The present sequence is that of the light chain of anti-  
CC indium-EDTA monoclonal antibody CHA255. As an example of the method of  
CC the invention, rational computer-aided design was used to develop an  
CC indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was  
CC to allow the chelate to bind non-covalently to CHA255 bound to a tumour  
CC and then to covalently attach the chelate to the antibody, thereby  
CC trapping it at the tumour site. This involved cloning the variable  
CC domains of CHA255 to construct a human/mouse chimeric Fab fragment that  
CC could be expressed in Escherichia coli, and the synthesis and screening  
CC of benzyl-EDTA chelates carrying weakly electrophilic groups capable of  
CC conjugation of the antibody in vivo. This Fab can be conjugated to a  
CC targeting moiety when desired. A reactive site was incorporated into the  
CC antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the  
CC light chain, near the region of the antibody to which the chelate bound.  
CC This was accomplished by site-directed mutagenesis of a nucleic acid  
CC encoding the wild-type of the anti-chelate antibody  
XX  
SQ Sequence 218 AA;

Query Match 98.9%; Score 1122; DB 4; Length 218;  
Best Local Similarity 99.5%; Pred. No. 2.3e-78;  
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPG 60  
Db 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPG 60  
QY 61 VPARFSGSLIGDKAALTTTGAQTEDEARFYCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120  
Db 61 VPARFSGSLIGDKAALTTTGAQTEDEARFYCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120  
QY 121 IFPPSPDLKSGTASVVCLANNYPVREAKVQWVDNALQSGNSQESVTEQDSKDSYISLS 180  
Db 121 IFPPSPDLKSGTASVVCLANNYPVREAKVQWVDNALQSGNSQESVTEQDSKDSYISLS 180  
QY 181 STLTSLKADYERKHVYACEVTHQGLSXPTKSFNRGEC 218  
Db 181 STLTSLKADYERKHVYACEVTHQGLSXPTKSFNRGEC 218

RESULT 3  
AAB20358  
ID AAB20358 standard; protein; 218 AA.  
XX  
AC AAB20358;  
XX  
XX 11-JUN-2001 (first entry)  
XX Anti-chelate antibody CHA255 light chain mutant N96C.  
XX Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;  
XX cancer; therapy; mutant; mutein.  
XX Mus musculus.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Region 1..23  
FT /label= FR1  
FT /note= "framework region 1"  
FT Region 24..37  
FT /label= CDR1  
FT /note= "complementarity determining region 1"  
FT Region 38..52  
FT /label= FR2  
FT /note= "framework region 2"  
FT Region 53..59  
FT /label= CDR2  
FT /note= "complementarity determining region 2"

FT Region 60..92  
FT /label= FR3  
FT /note= "framework region 3"  
FT Region 93..100  
FT /label= CDR3  
FT /note= "complementarity determining region 3"  
FT Misc-difference 96  
FT /note= "replaces Asn of wild-type sequence"  
FT Misc-difference 100  
FT /note= "encoded by GTR"  
FT Region 101..131  
FT /label= FR4  
FT /note= "framework region 4"  
FT Misc-difference 112  
FT /note= "encoded by CGW"  
FT Misc-difference 113  
FT /note= "encoded by ACK"  
FT Misc-difference 206  
FT /note= "encoded by AGY"  
FT Misc-difference 207  
FT /note= "encoded by TYG"  
XX  
XX WO200122922-A2.  
XX  
PD 05-APR-2001.  
XX  
XX 27-SEP-2000; 2000WO-US026619.  
XX  
XX 27-SEP-1999; 99US-0156194P.  
PR 31-MAY-2000; 2000US-0208684P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Meares C, Chmura A;  
PI  
XX WPI; 2001-244971/25.  
DR N-PSDB; AAF30633.  
XX  
XX Nucleic acid encoding a mutant antibody comprising a reactive site that  
FT specifically binds to a metal chelate useful as analytical agents and in  
FT clinical diagnosis, as well as in the treatment of disease, particularly  
FT cancer.  
XX  
XX Disclosure; Fig 12; 100pp; English.  
XX  
XX The invention provides a mutant antibody comprising a reactive site that  
CC is not present in the wild-type of the antibody. The antibody also has a  
CC complementarity determining region (CDR) that specifically binds to a  
CC metal chelate against which the wild-type antibody is raised. The  
CC reactive site of the mutant antibody is in a position proximate to or  
CC within the CDR, such that the chelate and the antibody are able to form a  
CC covalent bond. The present sequence is that of the light chain variable  
CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C  
CC mutation. As an example of the method of the invention, rational computer  
CC -aided design was used to develop an indium-EDTA chelate to covalently  
CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-  
CC covalently to CHA255 bound to a tumour and then to covalently attach the  
CC chelate to the antibody, thereby trapping it at the tumour site. This  
CC involved cloning the variable domains of CHA255 to construct a  
CC human/mouse chimeric Fab fragment that could be expressed in Escherichia  
CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying  
CC weakly electrophilic groups capable of conjugation of the antibody in  
CC vivo. This Fab can be conjugated to a targeting moiety when desired. A  
CC reactive site was incorporated into the antibody by engineering a Cys  
CC residue at location Asn-96 or Ser-95 of the light chain, near the region  
CC of the antibody to which the chelate bound. This was accomplished by site  
CC -directed mutagenesis of a nucleic acid encoding the wild-type of the  
CC anti-chelate antibody  
XX  
SQ Sequence 218 AA;

Query Match 98.1%; Score 1113; DB 4; Length 218;  
Best Local Similarity 99.1%; Pred. No. 1.1e-77;





PA (REGC ) UNIV CALIFORNIA.  
XX Meares C, Corneillie T;  
XX WPI; 2004-580725/56.  
DR N-PSDB; ADQ98055.  
XX Novel mutant antibody comprising reactive site not present in wild-type  
PT of antibody and antigen recognition domain that recognizes macrocyclic  
PT metal chelate having four nitrogen atoms, useful for treating cancer or  
PT autoimmune diseases.  
XX  
XX Claim 41; SEQ ID NO 28; 208pp; English.  
XX  
XX This invention relates to multi-functional antibodies that recognise  
CC chelating agents and metal chelates, particularly macrocyclic metal  
CC chelates. Specifically, it refers to an antibody that comprises a metal  
CC chelate bound to an antigen recognition domain, where the metal chelate  
CC has a reactive functional group of complementary reactivity to the  
CC reactive site of the antibody. This reactive site is the side chain of a  
CC naturally occurring amino acid e.g. the -SH group side chain of a  
CC cysteine residue (not present in the wild type) which can be used to form  
CC a covalent bond between the reactive site of the antibody and the  
CC reactive functional group of the metal chelate. The present invention  
CC describes using these antibodies for in vivo imaging where the antibody  
CC comprises a targeting moiety that binds specifically to a cell via a cell  
CC surface receptor or antigen thus forming a cell-mutant antibody complex.  
CC On addition of the metal chelate, a cell-antibody-metal chelate complex  
CC is formed that can be detected using emission tomography, magnetic  
CC resonance imaging, lanthanide luminescence, gamma-emissions or single  
CC photon emission tomography (SPET). As such, this method is useful for  
CC treating a subject with cancer and pharmaceutical compositions exhibit  
CC cytostatic and immunosuppressive activities. This polypeptide sequence is  
CC the chimeric mutant N53C murine antibody 2D12.5 variable light chain  
CC protein fused to the human anti-tetanus toxin antibody kappa light chain  
CC constant region of the invention.  
XX  
XX Sequence 218 AA;

Query Match 95.4%; Score 1082; DB 8; Length 218;  
Best Local Similarity 95.9%; Pred. No. 2,7e-75;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSYANVWQEKDPHFTGLIGTNNRPG 60  
DB 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSYANVWQEKDPHFTGLIGTNNRPPG 60  
QY 61 VPARFSGSLIGDKAALITGAQTEDEARYFCALWYCNLWVFGGTKLTVLSRTVAAPSVF 120  
DB 61 VPARFSGSLIGDKAALITGAQTEDEARYFCALWYCNLWVFGGTKLTVLSRTVAAPSVF 120  
QY 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180  
DB 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180  
QY 181 STLTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
DB 181 STLTSLKADYKHKVYACEVTHQGLSLPVTKSFNRGEC 218

RESULT 6  
ADR23362  
ID ADR23362 standard; protein; 215 AA.  
XX  
XX ADR23362;  
XX  
XX 04-NOV-2004 (first entry)  
XX Human CD72-targeted IgG1 light chain.  
XX Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;  
XX immunosuppressive; cancer; autoimmune disease; gene therapy.

OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Region 1..109  
FT /label= V\_region  
FT Region 110..215  
FT /label= C\_region  
XX WO2004067569-A1.  
XX 12-AUG-2004.  
XX 27-JAN-2003; 2003WO-EP050004.  
XX 27-JAN-2003; 2003WO-EP050004.  
XX (CRUC-) CRUCELL HOLLAND BV.  
XX Bakker ABH, Mariassen WE;  
XX WPI; 2004-580978/56.  
XX N-PSDB; ADR23361.  
XX New internalizing human binding molecules capable of specifically binding  
PT to CD72, useful for diagnosing and/or treating B-cell associated  
PT diseases, such as cancer or autoimmune disorders.  
XX Example 5; SEQ ID NO 54; 174pp; English.  
XX The present sequence is the protein sequence of the light chain of human  
CC IgG1 antibody 025, which specifically recognises human B cell associated  
CC antigen CD72. An scFv ADR23324 selected from an antibody phage display  
CC library was shown to specifically recognise the human CD72 receptor. The  
CC scFv was recloned in IGG expression vector C01 using primers designed to  
CC restore complete human frameworks, thereby generating antibody 025. Such  
CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used  
CC as internalising human binding molecules of the invention. These  
CC internalising human binding molecules are capable of (specifically)  
CC binding to CD72 or its antigenic determinant, and preferably bind to CD72  
CC associated with cells. Upon binding to CD72 present on the surface of  
CC target cells, the binding molecules internalise. In addition to the  
CC internalising human binding molecules, the invention provides  
CC immunocjugates comprising an internalising human binding molecule and a  
CC tag (toxic substance, radioactive substance, liposome and/or enzyme),  
CC nucleic acids encoding these, and compositions comprising them. The  
CC internalising human binding molecule, immunoconjugate, nucleic acid  
CC molecule or composition can be used in the diagnosis and/or treatment of  
CC a B cell associated disorder or disease, especially a B cell associated  
CC cancer and B cell associated autoimmune disorder (claimed).  
XX  
XX Sequence 215 AA;  
Query Match 68.7%; Score 779; DB 8; Length 215;  
Best Local Similarity 72.3%; Pred. No. 5.4e-52;  
Matches 162; Conservative 15; Mismatches 31; Indels 16; Gaps 4;  
QY 2 SAVVTQESALTTSPGETVTLTCRSSIGAVTTSYANVWQEKDPHFTGLIGTNNRPGV 61  
DB 1 SSELTDQPAVSVVALGQTVRITCQ---GDSLRSYASYWYQKPGQAPVLYVIGKNRRPSGI 57  
QY 62 PARFSGSLIGDKAALITGAQTEDEARYFCALWYCNL-----WVFGGTKLTVLSRTV 114  
DB 58 PDRFSGSSSGNTASLTITGAQDEADY-----YCNRSRDSGNHVVFGGTKLTVLG-TV 111  
QY 115 AAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK 174  
DB 112 AAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK 171  
QY 175 STYLSLSTLTSLKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
DB 172 STYLSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

```

RESULT 7
AAE27925
ID AAE27925 standard; protein; 235 AA.
XX
XX
AC AAE27925;
XX
XX
DT 27-DEC-2002 (first entry)
XX
XX
DE Human C2B8 antibody light chain protein.
XX
XX
KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200260955-A2.
XX
XX
PD 08-AUG-2002.
XX
XX
PF 29-JAN-2002; 2002WO-US002373.
XX
XX
PR 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
XX
XX
PA (IDEC-) IDEC PHARM CORP.
XX
XX
PI Braslawsky GR, Hanna N, Chinn P;
XX
XX
DR WPI; 2002-698547/75.
DR N-PSDB; AAD45754.
XX
XX
PT Novel domain deleted CC49 antibody reactive with tumor associated antigen
PT -72, or C2B8 antibody reactive with CD20, useful for treating
PT myelosuppressed patient suffering from a neoplastic disorder.
XX
XX
PS Example 1; Fig 3B; 74pp; English.
XX
XX
CC The present invention relates to domain deleted CC49 or C2B8 antibodies.
CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
CC deleted sequence in which CH2 domain has been deleted and are reactive
CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC with CD20 and comprise a heavy chain having a sequence of a derived
CC domain deleted C2B8 construct where the CH2 domain has been deleted.
CC Sequences of the invention are useful for imaging a neoplasm. They are
CC also useful for treating myelosuppressed patients suffering from
CC neoplastic disorder such as haematologic neoplasm, preferably non-
CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat
CC neoplastic disorder, colon cancer and haematologic malignancy. They are
CC useful for reducing tumour size, inhibiting tumour growth and/or
CC prolonging the survival time of tumour-bearing animals and for treating
CC tumours. The present sequence is human C2B8 light chain protein. This
CC sequence is used in the exemplification of the invention
XX
XX
SQ Sequence 235 AA;

Query Match 67.0%; Score 759.5; DB 5; Length 235;
Best Local Similarity 70.5%; Pred. No. 1.9e-50;
Matches 155; Conservative 16; Mismatches 42; Indels 7; Gaps 3;

QY 1 RSAVVTQES--ALTTSPGETVLTCSRSGIGAVTTSNANWVQEKPDHLFTGLIGTNNRA 58
Db 21 RQIVLSGSPAILSSAPGEKVTMTCRAS----SSVSYIHWFOQKPGSPKWIYATSNLA 76
QY 59 PGVPARFSGSLIGDKAALTTGAQTEDEARYFCALWYCNLWVFGGTTKLTVLRSRTVAAPS 118
Db 77 SGVPVRFSGSGSGTSSYLSITSRVEADAATYVCQWTSNPPTFGGTTKLEI-KRTVAAPS 135
QY 119 VFIPFSPDEQLSGTASVCLNNPYPREAKVQWKNALQSGNSQESVTEQDSKDSYTS 178
Db 136 VFIPFSPDEQLSGTASVCLNNPYPREAKVQWKNALQSGNSQESVTEQDSKDSYTS 195
QY 179 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEK 218

196 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEK 235
|||||
Db 196 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEK 235
|||||
RESULT 8
ABB82834
ID ABB82834 standard; protein; 235 AA.
XX
XX
AC ABB82834;
XX
XX
DT 31-MAR-2003 (first entry)
XX
XX
DE Antibody C2B8 light chain.
XX
XX
KW C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW thymimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW dermatological; immunosuppressive; antiinflammatory.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200296948-A2.
XX
XX
PD 05-DEC-2002.
XX
XX
PF 29-JAN-2002; 2002WO-US002374.
XX
XX
PR 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
PR 21-DEC-2001; 2001US-0341858P.
XX
XX
PA (IDEC-) IDEC PHARM CORP.
XX
XX
PI Braslawsky GR, Hanna N, Chinn P, Hariharan K;
XX
XX
DR WPI; 2003-140446/13.
DR N-PSDB; ABZ24018.
XX
XX
PT Novel dimeric antibody useful for treating immune disorder and neoplastic
PT disorder, has several non-covalently associated monomeric subunits.
XX
XX
PS Example 1; Fig 3B; 78pp; English.
XX
XX
CC The invention relates to a dimeric antibody (I) comprising several
CC monomeric subunits, where the monomeric subunits are non-covalently
CC associated. (I) is useful for treating a disorder, especially immune
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC resistant Hodgkin's disease high grade, low grade and intermediate grade
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
CC detailed description of the various uses of (I)). The present sequence
CC represents the antibody C2B8 light chain
XX
XX
SQ Sequence 235 AA;

Query Match 67.0%; Score 759.5; DB 6; Length 235;
Best Local Similarity 70.5%; Pred. No. 1.9e-50;
Matches 155; Conservative 16; Mismatches 42; Indels 7; Gaps 3;

QY 1 RSAVVTQES--ALTTSPGETVLTCSRSGIGAVTTSNANWVQEKPDHLFTGLIGTNNRA 58
Db 21 RQIVLSGSPAILSSAPGEKVTMTCRAS----SSVSYIHWFOQKPGSPKWIYATSNLA 76
QY 59 PGVPARFSGSLIGDKAALTTGAQTEDEARYFCALWYCNLWVFGGTTKLTVLRSRTVAAPS 118
Db 77 SGVPVRFSGSGSGTSSYLSITSRVEADAATYVCQWTSNPPTFGGTTKLEI-KRTVAAPS 135

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QY 119 VFIPPSDQLKSGTASVVCLLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSYSTS 178
DB 136 VFIPPSDQLKSGTASVVCLLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSYSTS 195
QY 179 LSSTLTSLKADYKHKVYACEVTHOGLSXPVTKSFNRGEC 218
DB 196 LSSTLTSLKADYKHKVYACEVTHOGLSXPVTKSFNRGEC 235

RESULT 9
ADL92471
ID ADL92471 standard; protein; 213 AA.
XX
AC ADL92471;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antibody "Rituximab" light chain sequence.
XX
KW cytostatic; antiinflammatory; cardiovascular; gene therapy; antibody; Fc;
KW agriculture; industrial application.
XX
OS Homo sapiens.
XX
FN WO2004029207-A2.
XX
PD 08-APR-2004.
XX
PF 26-SEP-2003; 2003WO-US030249.
XX
PR 27-SEP-2002; 2002US-0414433P.
PR 23-JAN-2003; 2003US-0442301P.
PR 02-MAY-2003; 2003US-0467606P.
PR 12-JUN-2003; 2003US-0477839P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Chirino AJ, Dang W, Desjarlais JR, Doberstein SK;
PI Hayes RJ, Karki SB, Vafa O;
XX
WPI; 2004-316096/29.
XX
XX
PT New optimized Fc variant antibody useful for diagnosing or treating
PT diseases (e.g. cancer, inflammation or cardiovascular diseases), in
PT research and in agricultural or industrial applications.
XX
XX
PS Example 12; Fig 31a; 192pp; English.
XX
CC The invention relates to an antibody comprising an Fc variant portion
CC having an amino acid modification in the Fc region of the parent Fc
CC polypeptide, where the Fc variant modulates binding to an Fc-gamma-R
CC compared to the parent Fc polypeptide. The antibody may also be used in
CC research and in agricultural or industrial applications. This sequence
CC corresponds to the light chain of the antibody "Rituximab" as an example
CC of an antibody of the invention.
XX
SQ Sequence 213 AA;

Query Match 66.9%; Score 759; DB 8; Length 213;
Best Local Similarity 71.8%; Pred. No. 1.9e-50;
Matches 155; Conservative 16; Mismatches 39; Indels 6; Gaps 3;

QY 4 VVTQESA-LTTSFGETVLTCSRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
DB 3 VLQSQPAILSASPGKVTMTCRAS----SSVSYIHWFQKPGSPKPMIYATSNLASGVP 58
QY 63 ARFGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPSVFIF 122
DB 59 VRFGSGSGTSYSLTISRVEADAATYTCQWTSNPPPTFGGKTKLEI-KRTVAAPSVFIF 117
QY 123 PPSDEQLKSGTASVVCLLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSYSTS 182
```

```
DB 118 PPSDEQLKSGTASVVCLLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSYSTS 177
QY 183 LTLSKADYKHKVYACEVTHOGLSXPVTKSFNRGEC 218
DB 178 LTLSKADYKHKVYACEVTHOGLSXPVTKSFNRGEC 213

RESULT 10
AAW82740
ID AAW82740 standard; protein; 235 AA.
XX
AC AAW82740;
XX
DT 10-MAY-1999 (first entry)
XX
DE Plasmid pNG3/ASB7VK-HuCK-NEO protein.
XX
KW Conjugate; cell targeting; cytotoxic drug; prodrug therapy system;
KW prodrug-converting enzyme; cell surface antigen; treatment; cancer;
KW inflammation; rheumatoid arthritis; antibody.
XX
OS Synthetic.
XX
FN WO9851787-A2.
XX
PD 19-NOV-1998.
XX
PF 05-MAY-1998; 98WO-GB001294.
XX
PR 10-MAY-1997; 97GB-00009421.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Emery SC, Blakey DC;
XX
WPI; 1999-059700/05.
DR N-PSDB; AAV72047.
XX
XX
PT New gene construct expressing conjugate of targeting agent and prodrug-
PT converting enzyme - useful for, e.g. targeted production of cytotoxic
PT drug in vivo, especially for treatment of cancer.
XX
PS Example 1f; Page 70; 100pp; English.
XX
CC This sequence is used in a method for obtaining a novel gene construct
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-
CC targeting group (I) and a heterologous prodrug-converting enzyme (II),
CC and (B) is directed to leave the cell for selective localisation at a
CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target
CC site, then administration of (III) is used for targeted release of
CC cytotoxic drug, specifically for treating cancer but also inflammation
CC such as rheumatoid arthritis. In situ generation of the targeting
CC antibody increases selectivity, reducing side effects at normal tissue.
CC The method is applicable to any antibody-directed enzyme prodrug therapy
XX
SQ Sequence 235 AA;

Query Match 66.8%; Score 757; DB 2; Length 235;
Best Local Similarity 71.8%; Pred. No. 3e-50;
Matches 155; Conservative 15; Mismatches 40; Indels 6; Gaps 3;

QY 4 VVTQESA-LTTSFGETVLTCSRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
DB 25 VLQSQPAILSASPGKVTMTCRAS----SSVTIHWYQKPGSPKSWIYATSNLASGVP 80
QY 63 ARFGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPSVFIF 122
DB 81 ARFGSGSGTSYSLTISRVEADAATYTCQHWSSKPTFGGKTKLEI-KRTVAAPSVFIF 139
QY 123 PPSDEQLKSGTASVVCLLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSYSTS 182
DB 140 PPSDEQLKSGTASVVCLLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSYSTS 199
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QY 193 LTLKADYKHKVYACEVTHQGLSKPVTYKSFNRGEC 218  
 DB 200 LTLKADYKHKVYACEVTHQGLSKPVTYKSFNRGEC 235

RESULT 11  
 AAB08025 ID AAB08025 standard; protein; 235 AA.  
 AC AAB08025;  
 XX  
 XX 12-SEP-2003 (revised)  
 DT 14-NOV-2000 (first entry)  
 XX

A dimeric anti-CD20 light chain polypeptide.

KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;  
 KW complement system; Fc gamma receptor; cytotoxic effector cell;  
 KW host immune cell; programmed cell death; allergic disorder; cancer;  
 KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;  
 KW allergic bronchopulmonary aspergillosis; allergic rhinitis;  
 KW Graves's disease; food allergy; allergic contact dermatitis; cancer;  
 KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;  
 KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;  
 KW diabetes mellitus; candidiasis; aplastic anaemia.  
 XX

OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX

FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /note= "signal peptide"  
 FT Protein 23..128  
 FT /note= "murine anti-human CD20 variable light chain"  
 FT Protein 129..235  
 FT /note= "human kappa light chain constant region"  
 XX

WO200044788-A1.  
 03-AUG-2000.  
 28-JAN-2000; 2000WO-US001893.  
 28-JAN-1999; 99US-00238741.  
 (IDBC-) IDEC PHARM CORP.  
 Braislawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;  
 WPI; 2000-514811/46.  
 DR N-PSDB; AAA63530.  
 XX Genetically engineering immunoglobulin (Ig) G/IgG dimers for the  
 PT treatment of cancers, allergic disorders and autoimmune conditions.  
 XX  
 PS Example 1; Fig 1A-B; 65pp; English.  
 XX

The present sequence represents a dimeric anti-CD20 light chain polypeptide. The dimeric immunoglobulin is used in the method of the invention. The specification describes a method for producing an immunoglobulin (Ig) G/IgG dimer. The method comprises genetically engineering a monoclonal antibody to introduce a cysteine molecule which inhibits formation of intramolecular disulphide bridges between sister heavy chains on the same antibody molecule. The dimer is a homodimer or heterodimer that is capable of activating components of the complement system, and has the ability to activate and kill cells via the complement cascade. The dimer is also capable of binding to Fc gamma receptors on cytotoxic effector cells and on host immune cells, and is capable of initiating programmed cell death. The IgG/IgG dimers may be used to treat allergic disorders, cancers and autoimmune diseases such as allergic asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis, CC

CC atopic dermatitis, Crohn's disease, Graves's disease, food allergies, CC allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They may also be used to treat a range of other diseases and disorders such as CC rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis CC and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected CC cell populations. (Updated on 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 235 AA;  
 Query Match 66.5%; Score 754.5; DB 3; Length 235;  
 Best Local Similarity 70.0%; Pred. No. 4.6e-50;  
 Matches 154; Conservative 16; Mismatches 43; Indels 7; Gaps 3;  
 XX

QY 1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRA 58  
 DB 21 RQIVLSQSPAILLSASPGKVTMTCRAS---SSVSYIHWFOQKPGSPKRWIVATSNLA 76  
 QY 59 PGVPARFSGSLIGDKAALITITGAQTEDEARYFCALWYCNLWVFGGTKLTVLSRTVAAPS 118  
 DB 77 SGVPVRFSGSGSGTSYSLTISRVEADAATYTCQOMTSNPPTFGGAKLEI-KRTVAAPS 135  
 QY 119 VFIFPPSDEQLKSGTASVCLLNPFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDSSTYS 178  
 DB 136 VFIFPPSDEQLKSGTASVCLLNPFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDSSTYS 195  
 QY 179 LSSTLTLSKADYKHKVYACEVTHQGLSKPVTYKSFNRGEC 218  
 DB 196 LSSTLTLSKADYKHKVYACEVTHQGLSKPVTYKSFNRGEC 235

RESULT 12  
 AAE34878 ID AAE34878 standard; protein; 213 AA.  
 XX  
 AC AAE34878;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE BIWA4/8 antibody light chain mature protein.  
 XX  
 KW BIWA8 antibody; heavy chain variable region; light chain variable region;  
 KW VH; VL; CD44v6; medicament; cancer; antibody therapy.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200294879-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 17-MAY-2002; 2002WO-EP005467.  
 XX  
 PR 18-MAY-2001; 2001EP-00112237.  
 XX  
 PR 26-SEP-2001; 2001US-0325147P.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
 XX  
 XX Adolf G, Ostermann E, Patzelt E, Sproll M, Heider K;  
 PI Miglietta JJ, Van Dongen AAMS;  
 XX  
 XX WPI; 2003-129413/12.  
 DR N-PSDB; AAD53214, AAD53217.  
 XX

New antibodies specific for an epitope coded by the variant exon of the CD44 gene, useful for treating cancer, including non-small cell lung, PT breast, head and neck, ovarian and lung cancer.  
 PT  
 XX Claim 26; Col 44; 78pp; English.  
 PS The present invention relates to novel antibody molecules comprising a CC variable region of the heavy (VH) and/or light chain (VL) of CD44v6



XX PS Claim 7; SEQ ID NO 8; 42pp; English.

XX CC The present invention describes using a compound (CD) of formula A(LB)n, where A is an antibody molecule which is specific for CD44, L is a linker moiety, B is a compound which is toxic to cells, and n is a decimal number between 1-10, for the preparation of a pharmaceutical composition for the treatment of cancer, where CD is used or is for use in combination with radiotherapy. Also described: (1) use of a conjugate (CJ) of a CD44v6 specific antibody molecule and a maytansinoid for the manufacture of a pharmaceutical composition for the treatment of cancer, where CJ is used or is for use in combination with radiotherapy; (2) a pharmaceutical composition comprising CD or CJ together with a radioimmunotherapeutic agent and optionally further comprising one or more carrier(s), diluent(s), or excipient(s); (3) a kit comprising, in a separate pharmaceutical composition, CD or CJ and a radioimmunotherapeutic agent; and (4) use of radioimmunotherapeutic agent (RA) for the preparation of a pharmaceutical composition for the treatment of cancer, where the radioimmunotherapeutic agent is used or is for use in combination with CD or CJ. CD and CJ have cytostatic activities, and can be used as immunostimulators. CJ is useful for the manufacture of a medicament for the treatment of cancer e.g. head and neck squamous cell carcinoma, oesophagus squamous cell carcinoma, lung squamous cell carcinoma, skin squamous cell carcinoma, cervix squamous cell carcinoma, breast adenocarcinoma, lung adenocarcinoma, pancreas adenocarcinoma, colon adenocarcinoma, and stomach adenocarcinoma. CD and CJ are useful for preparation of a pharmaceutical composition for the treatment of cancer. CD and CJ are useful for treating cancer in a patient which involves administering CD or CJ to the patient in combination with radiotherapy. CD and CJ are useful as an adjuvant to surgical interaction, to treat minimal residual disease. The present sequence represents a humanised murine antibody BIWA 8 light chain, which is used in the exemplification of the present invention.

XX SQ Sequence 213 AA;

Query Match 66.4%; Score 753; DB 8; Length 213;  
 Best Local Similarity 72.2%; Pred. No. 5.4e-50;  
 Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

QY 4 VVQESA-LTTPSGETVTLTCRSSIGAVTTSNYANWVQEKDPDLFTGLIGGTNNRAGVP 62  
 Db 3 VLTQSPATLSLSPGERATLSCAS----SSINYYWVQKPGQAPRLIYLTLNLSAGVP 58

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLVLSRTVAAPSVFIF 122  
 Db 59 ARFSGSGGTDFTLTISLEPEDFAVYCYCLOWSSNPLTFGGGTKEI-KRTVAAPSVFIF 117

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 182  
 Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 177

QY 183 LTLSKADYERKHVKYACEVTHQGLSXPTKSFNRGEC 218  
 Db 178 LTLSKADYERKHVKYACEVTHQGLSSPTKSFNRGEC 213

RESULT 15  
 AAEE35326  
 ID AAEE35326 standard; protein; 213 AA.

XX AC AAEE35326;

XX DT 17-JUN-2003 (first entry)

XX DE Humanised murine antibody BIWA4 light chain protein.

XX KW CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease;  
 XX antigen; cytostatic; BIWA4 antibody; murine.

XX OS Homo sapiens.

XX PN EP1250255-A1.

XX PD 20-NOV-2002.

XX PF 18-MAY-2001; 2001EP-00112227.

XX PR 18-MAY-2001; 2001EP-00112227.

XX PA (BOBH ) BOEHRINGER INGELHEIM INT GMBH.

XX PI Adolf G, Heider K, Patzelt E, Sproll M;

XX DR WPI; 2003-177273/18.

XX DR N-PSDB; RAD53976.

XX CC New compound useful for treatment of cancer comprises CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions.

XX PS Claim 7; Page 14; 31pp; English.

XX CC The invention relates to a compound comprising CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions. The compound is used in pharmaceutical composition for the treatment of cancer, solid tumours, and as an adjuvant to surgical intervention to treat minimal residual disease. The present sequence is humanised murine antibody BIWA4 light chain protein used in the invention

XX SQ Sequence 213 AA;

Query Match 66.2%; Score 751; DB 6; Length 213;  
 Best Local Similarity 72.2%; Pred. No. 7.6e-50;  
 Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;

QY 4 VVQESA-LTTPSGETVTLTCRSSIGAVTTSNYANWVQEKDPDLFTGLIGGTNNRAGVP 62  
 Db 3 VLTQSPATLSLSPGERATLSCAS----SSINYYWVQKPGQAPRLIYLTLNLSAGVP 58

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLVLSRTVAAPSVFIF 122  
 Db 59 ARFSGSGGTDFTLTISLEPEDFAVYCYCLOWSSNPLTFGGGTKEI-KRTVAAPSVFIF 117

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 182  
 Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 177

QY 183 LTLSKADYERKHVKYACEVTHQGLSXPTKSFNRGEC 218  
 Db 178 LTLSKADYERKHVKYACEVTHQGLSSPTKSFNRGEC 213

Search completed: June 7, 2005, 15:54:04  
 Job time : 115.5 secs

	Query Match	66.8%; Score 757; DB 3; Length 235;
	Best Local Similarity	71.8%; Pred.No. 7.9e-67;
	Matches	Conservative 15; Mismatches 40; Indels 6; Gaps 3;
Qy	4 VVTDSEA-LITTSGETVLTCRSSIGAVTTSNYANWYQEKPDLHLFTGLTGTTNNRAPGVP	62
Dd	25 VLGSPPALNSAGEKVTMTCRAS---SSVTYLHWYQQKGSPSKSWIYATSNLASGVP	80
Qy	63 ARFGSLHGKAALTITGAOTEDEARFYCALWYNCLNVFEGGTKLTVLSRTVAAPSVEIF	122

Db 81 ARFGSGSGTSYSLTISRVEADAATYYCQHWSKPPTFGGTKLEI-KRTVAAPSVPIF 139  
Qy 123 PPSDEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLST 182  
Db 140 PPSDEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLST 199  
Qy 163 LTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218  
Db 200 LTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 235

## RESULT 2

US-08-952-235-1  
; Sequence 1, Application US/08952235  
; Patent No. 6207152  
; GENERAL INFORMATION:  
; APPLICANT: Schwall, Ralph H.  
; APPLICANT: Tabor, Kelly H.  
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
; TITLE OF INVENTION: Antagonists and Uses Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,235  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-952-235-1

Query Match 66.1%; Score 750; DB 3; Length 220;

Best Local Similarity 71.8%; Pred. No. 3.6e-66;  
Matches 153; Conservative 13; Mismatches 43; Indels 4; Gaps 2;

Qy 9 SALTTSPEGTVLTCSRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAGVPARF 65  
Db 9 SSLTVSVEKVTVSKSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTRESGVDPDRF 68  
Qy 66 SGSLIGDKAALTTTGAQTEDEARYFCALWYCNLWVFGGCTKLTVLSRTVAAPSVFIIPPS 125  
Db 69 TGSQSGTDFTLTITSVKADDLAVVYCOQYAYPWTFGGKTLEI-KRTVAAPSVFIIPPS 127  
Qy 126 DEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 185  
Db 128 DEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 187

Qy 186 SKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218  
Db 188 SKADYKHKVYACEVTHQGLSPVTKSFNRGEC 220

## RESULT 3

US-09-669-971-1  
; Sequence 1, Application US/09669971  
; Patent No. 6468529  
; GENERAL INFORMATION:  
; APPLICANT: Schwall, Ralph H.  
; APPLICANT: Tabor, Kelly H.  
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
; TITLE OF INVENTION: Antagonists and Uses Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/669,971  
; FILING DATE: 05-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,235  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-669-971-1

Query Match 66.1%; Score 750; DB 4; Length 220;  
Best Local Similarity 71.8%; Pred. No. 3.6e-66;  
Matches 153; Conservative 13; Mismatches 43; Indels 4; Gaps 2;

Qy 9 SALTTSPEGTVLTCSRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAGVPARF 65  
Db 9 SSLTVSVEKVTVSKSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTRESGVDPDRF 68  
Qy 66 SGSLIGDKAALTTTGAQTEDEARYFCALWYCNLWVFGGCTKLTVLSRTVAAPSVFIIPPS 125  
Db 69 TGSQSGTDFTLTITSVKADDLAVVYCOQYAYPWTFGGKTLEI-KRTVAAPSVFIIPPS 127  
Qy 126 DEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 185  
Db 128 DEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 187  
Qy 186 SKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218  
Db 188 SKADYKHKVYACEVTHQGLSPVTKSFNRGEC 220

## RESULT 4

US-09-472-087-15  
; Sequence 15, Application US/09472087  
; Patent No. 6682736



```

; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-15

Query Match 65.5%; Score 743; DB 4; Length 233;
Best Local Similarity 70.4%; Pred. No. 1.9e-65;
Matches 152; Conservative 19; Mismatches 39; Indels 6; Gaps 3;

Qy 4 VVTQE-SALTTSPEETVLTLCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPGVP 62
Db 23 VLTQSPGTLSSLSPGERATLSCRTSV----SSSYLAWYQQKPGQAPRLIIYGASSRATGIP 78
Qy 63 ARPSGSLIGDKAALTIITGAOTEDEARFYFCALWYCNLWVFGGCTKLTVLRSRTVAAPSVFIF 122
Db 79 DRFGSGSGTGDTFTLTISRLPEDFAVYVCQYGGISPTFTGGTKVEI-KRTVAAPSVFIF 137
Qy 123 PPSDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSST 182
Db 138 PPSDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSST 197
Qy 183 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 218
Db 198 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 233

RESULT 5
US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-67

Query Match 65.5%; Score 743; DB 4; Length 233;
Best Local Similarity 70.4%; Pred. No. 1.9e-65;
Matches 152; Conservative 19; Mismatches 39; Indels 6; Gaps 3;

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Db 60 PPSGSGSTDTLTISSLPQDFDTYYCQWSSNPPPTFGGKTKEI-KRTVAASVFIIP 118  
QY 124 PSDEQLKSGTASVCLLNFPYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLSTL 183  
Db 119 PSDEQLKSGTASVCLLNFPYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLSTL 178  
QY 184 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 179 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 213

## RESULT 7

US-09-011-769A-27

; Sequence 27, Application US/09011769A

; Patent No. 6436691

; GENERAL INFORMATION:

; APPLICANT: SLATER, Anthony M.

; BLAKEY, David C.

; DAVIES, David H.

; HENNAM, John F.

; HENNEQUIN, Laurent F.A.

; MARSHAM, Peter R.

; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison &amp; Sutro, LLP

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/011,769A

; FILING DATE: 13-Feb-1998

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB96/01975

; FILING DATE: 13-AUG-1996

; APPLICATION NUMBER: GB 9612295.7

; FILING DATE: 12-JUN-1996

; APPLICATION NUMBER: GB 9611019.2

; FILING DATE: 25-MAY-1996

; APPLICATION NUMBER: GB 9516810.0

; FILING DATE: 16-AUG-1995

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 235 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-011-769A-27

Db 60 PPSGSGSTDTLTISSLPQDFDTYYCQWSSNPPPTFGGKTKEI-KRTVAASVFIIP 118  
QY 124 PSDEQLKSGTASVCLLNFPYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLSTL 183  
Db 119 PSDEQLKSGTASVCLLNFPYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLSTL 178  
QY 184 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 179 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 213

## RESULT 7

US-09-011-769A-27

; Sequence 27, Application US/09011769A

; Patent No. 6436691

; GENERAL INFORMATION:

; APPLICANT: SLATER, Anthony M.

; BLAKEY, David C.

; DAVIES, David H.

; HENNAM, John F.

; HENNEQUIN, Laurent F.A.

; MARSHAM, Peter R.

; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison &amp; Sutro, LLP

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/011,769A

; FILING DATE: 13-Feb-1998

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB96/01975

; FILING DATE: 13-AUG-1996

; APPLICATION NUMBER: GB 9612295.7

; FILING DATE: 12-JUN-1996

; APPLICATION NUMBER: GB 9611019.2

; FILING DATE: 25-MAY-1996

; APPLICATION NUMBER: GB 9516810.0

; FILING DATE: 16-AUG-1995

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 235 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-011-769A-27

Db 140 PPSDEQLKSGTASVCLLNFPYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 199  
QY 183 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 200 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 235

## RESULT 8

US-09-315-926A-79

; Sequence 79, Application US/09315926A

; Patent No. 6498027

; GENERAL INFORMATION:

; APPLICANT: Es van, Helmut

; APPLICANT: Havenga, Menzo

; APPLICANT: Verlinden, Stefan

; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

; FILE REFERENCE: 2183-4080US

; CURRENT APPLICATION NUMBER: US/09/315,926A

; CURRENT FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 99201593.3

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 98201693.3

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 79

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Description of Artificial Sequence: phage

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(236)

; OTHER INFORMATION: /note="hCAT1 amino acid sequence"

US-09-315-926A-79

Db 140 PPSDEQLKSGTASVCLLNFPYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 199  
QY 183 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 200 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 235

## RESULT 8

US-09-315-926A-79

; Sequence 79, Application US/09315926A

; Patent No. 6498027

; GENERAL INFORMATION:

; APPLICANT: Es van, Helmut

; APPLICANT: Havenga, Menzo

; APPLICANT: Verlinden, Stefan

; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

; FILE REFERENCE: 2183-4080US

; CURRENT APPLICATION NUMBER: US/09/315,926A

; CURRENT FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 99201593.3

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 98201693.3

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 79

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Description of Artificial Sequence: phage

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(236)

; OTHER INFORMATION: /note="hCAT1 amino acid sequence"

US-09-315-926A-79

Db 140 PPSDEQLKSGTASVCLLNFPYPREAKVQWVDNALQSGNSQESVTEQDSKDYSLST 199  
QY 183 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 200 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 235

## RESULT 8

US-09-315-926A-79

; Sequence 79, Application US/09315926A

; Patent No. 6498027

; GENERAL INFORMATION:

; APPLICANT: Es van, Helmut

; APPLICANT: Havenga, Menzo

; APPLICANT: Verlinden, Stefan

; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

; FILE REFERENCE: 2183-4080US

; CURRENT APPLICATION NUMBER: US/09/315,926A

; CURRENT FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 99201593.3

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 98201693.3

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 79

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Description of Artificial Sequence: phage

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(236)

; OTHER INFORMATION: /note="hCAT1 amino acid sequence"

US-09-315-926A-79

```
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-17

Query Match      64.6%; Score 732.5; DB 4; Length 234;
Best Local Similarity 69.9%; Pred. No. 2.1e-64;
Matches 151; Conservative 18; Mismatches 42; Indels 5; Gaps 3;

QY 4 VVTQES-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHFLTGLIGGTNNRAGVP 62
DB 23 VLTQSPGTLSPGERATLSCRAS---QSVSSYLAWYQKPGQAPRPLIYGVSSRATGIP 79

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGKTKLTVLSRTVAAPSVFIF 122
DB 80 DRFGSGSGTDTLTISRLEPEDFAVYQCQYIGSPFTFGPGTKVDI-KRTVAAPSVFIF 138

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 182
DB 139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 198

QY 183 LTLKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
DB 199 LTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 10
US-09-472-087-69
; Sequence 69, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-69

Query Match      64.6%; Score 732.5; DB 4; Length 234;
Best Local Similarity 69.9%; Pred. No. 2.1e-64;
Matches 151; Conservative 18; Mismatches 42; Indels 5; Gaps 3;

QY 4 VVTQES-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHFLTGLIGGTNNRAGVP 62
DB 23 VLTQSPGTLSPGERATLSCRAS---QSVSSYLAWYQKPGQAPRPLIYGVSSRATGIP 79

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGKTKLTVLSRTVAAPSVFIF 122
DB 80 DRFGSGSGTDTLTISRLEPEDFAVYQCQYIGSPFTFGPGTKVDI-KRTVAAPSVFIF 138

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 182
DB 139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 198

QY 183 LTLKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
DB 199 LTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 11
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match      64.6%; Score 732; DB 4; Length 235;
Best Local Similarity 69.4%; Pred. No. 2.3e-64;
Matches 150; Conservative 19; Mismatches 43; Indels 4; Gaps 3;

QY 4 VVTQES-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHFLTGLIGGTNNRAGVP 62
DB 23 VLTQSPGTLSPGERATLSCRAS---QSVSSYLAWYQKPGQAPRPLIYGVSSRATGIP 80

QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGKTKLTVLSRTVAAPSVFIF 122
DB 81 DRFGSGSGTDTLTISRLEPEDFAVYQCQYIGSPFTFGPGTKVDI-KRTVAAPSVFIF 139

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 182
DB 140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLST 199

QY 183 LTLKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
DB 200 LTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 12
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
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Qy 64 RFGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGTKLTVLSTVAAPSVFIIP 123  
Db 84 RFGSGSGTDYTLTISLQPEDFATYCYQYSTVPWTFQGQTKVEI-KRTVAAPSVFIIP 142  
Qy 124 PSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL 183  
Db 143 PSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL 202  
Qy 184 TLKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218  
Db 203 TLKADYKHKVYACEVTHQGLSSPTKSFNRGEC 237

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Job time : 30.5 secs

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QY	1	RS	AV	VT	Q	E	S	A	L	T	T	P	G	E	T	V	T	L	T	C	R	S	S	G	A	V	T	S	N	Y	A	N	N	V	Q	E	K	P	D	H	L	F	T	G	L	I	G	G	T	N	N	R	A	P	G	60				
ph	1	RS	AV	VT	Q	E	S	A	L	T	T	P	G	E	T	V	T	L	T	C	R	S	S	G	A	V	T	S	N	Y	A	N	N	V	Q	E	K	P	D	H	L	F	T	G	L	I	G	G	T	N	N	R	A	P	G	60				

QY 61 VPAFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPSVP 120  
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QY 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 180  
DB 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 180  
QY 181 STLTLSKADYEHKHYACEVTHQGLSPVTKSFNRGEC 218  
DB 181 STLTLSKADYEHKHYACEVTHQGLSPVTKSFNRGEC 218

## RESULT 2

US-10-625-047-28  
Query Match 95.4%; Score 1082; DB 16; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.3e-84;  
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Meares, Claude  
APPLICANT: Corneillie, Todd  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Multi-Functional Antibodies  
FILE REFERENCE: 023070-130910US  
CURRENT APPLICATION NUMBER: US/10/625,047  
CURRENT FILING DATE: 2003-07-22  
PRIOR APPLICATION NUMBER: US 10/350,555  
PRIOR FILING DATE: 2003-01-23  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:N53C cloned  
OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable  
OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin  
OTHER INFORMATION: antibody kappa light chain constant region (ITCL)  
US-10-625-047-28

QY 1 RSAVVTQESALTTSFGETVTLTCRSSIGAVTTSNYANNVQEKPDHLFTGLIGGTNNRAPG 60  
DB 1 RSAVVTQESALTTSFGETVTLTCRSSIGAVTTSNYANNVQEKPDHLFTGLIGGTNNRAPG 60  
QY 61 VPAFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPSVP 120  
DB 61 VPAFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPSVP 120  
QY 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 180  
DB 121 IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 180  
QY 181 STLTLSKADYEHKHYACEVTHQGLSPVTKSFNRGEC 218  
DB 181 STLTLSKADYEHKHYACEVTHQGLSPVTKSFNRGEC 218

## RESULT 3

US-10-723-003-42  
Query Match 66.4%; Score 753; DB 14; Length 213;  
Best Local Similarity 72.2%; Pred. No. 1.9e-56;  
Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;  
GENERAL INFORMATION:  
APPLICANT: MA, Jing  
APPLICANT: GUO, Yajun  
TITLE OF INVENTION: PREPARATION AND APPLICATION OF  
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS  
FILE REFERENCE: 549062000200  
CURRENT APPLICATION NUMBER: US/10/723,003  
CURRENT FILING DATE: 2003-11-26

QY 1 RSAVVTQESALTTSFGETVTLTCRSSIGAVTTSNYANNVQEKPDHLFTGLIGGTNNRA 58  
DB 21 RQIVLSQSPAILSSASPEGEKVTMTCRAS----SSVSIHWFQQKPGSPKRWIYATSLA 76  
QY 59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPS 118  
DB 77 SGVPEVRFSGSGGTSYSLTISRVEADAATYCCQWTSNPPTFGGKLEI-KRTVAAPS 135  
QY 119 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 178  
DB 136 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 195  
QY 179 LSSTLTLSKADYEHKHYACEVTHQGLSPVTKSFNRGEC 218  
DB 196 LSSTLTLSKADYEHKHYACEVTHQGLSPVTKSFNRGEC 235

Query Match 67.0%; Score 759.5; DB 16; Length 235;  
Best Local Similarity 70.5%; Pred. No. 5.8e-57;  
Matches 155; Conservative 16; Mismatches 42; Indels 7; Gaps 3;  
GENERAL INFORMATION:  
APPLICANT: Meares, Claude  
APPLICANT: Corneillie, Todd  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Multi-Functional Antibodies  
FILE REFERENCE: 023070-130910US  
CURRENT APPLICATION NUMBER: US/10/625,047  
CURRENT FILING DATE: 2003-07-22  
PRIOR APPLICATION NUMBER: US 10/350,555  
PRIOR FILING DATE: 2003-01-23  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-723-003-42

US-10-150-475A-8  
Query Match 66.4%; Score 753; DB 14; Length 213;  
Best Local Similarity 72.2%; Pred. No. 1.9e-56;  
Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;  
GENERAL INFORMATION:  
APPLICANT: Adolf, G. et al.  
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates  
FILE REFERENCE: 1/1211  
CURRENT APPLICATION NUMBER: US/10/150,475A  
CURRENT FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: US 60/307,451  
PRIOR FILING DATE: 2001-07-24  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Humanised  
OTHER INFORMATION: Murine Antibody BiWA 8 Light Chain SEQ ID NO: 8  
US-10-150-475A-8

QY 4 VVTQESA-LTTSFGETVTLTCRSSIGAVTTSNYANNVQEKPDHLFTGLIGGTNNRAPGVP 62  
DB 3 VLTQSPATLSLSPGERATLSCSAS----SSNIYIWLQQKPGQAPRLIYLTSLNASGVP 58  
QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPSVP 122  
DB 59 ARFSGSGSGTDFLTITISLPEDEFAVYCYCLOWSSNPPLTFGGTKVEI-KRTVAAPSVP 117  
QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 182  
DB 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 177



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QY 183 LTLSKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 178 LTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGEC 213

RESULT 5
US-10-704-522-8
; Sequence 8, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Humanised Murine Antibody BIWA 8 Light Chain
US-10-704-522-8

Query Match 66.4%; Score 753; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 1.9e-56;
Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

QY 4 VVTQESA-LTTSPEGTVTLTCRSSIGAVTTSYANNVQKPDHLFTGLIGGTNNRAGVP 62
Db 3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYLQKPGQAPRIILYLTSLNLAGVP 58

QY 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYCNLWVFGGKTKLTVLSRTVAAPSVFIF 122
Db 59 ARFSGSGGTDFTLTITSSLEPEDFAVYICLWSSNPLTFGGGKVEI-KRTVAAPSVFIF 117

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 177

QY 183 LTLSKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 178 LTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGEC 213

RESULT 6
US-10-645-215-8
; Sequence 8, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-10-645-215-8

Query Match 66.4%; Score 753; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 1.9e-56;
Matches 156; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

QY 4 VVTQESA-LTTSPEGTVTLTCRSSIGAVTTSYANNVQKPDHLFTGLIGGTNNRAGVP 62
Db 3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYLQKPGQAPRIILYLTSLNLAGVP 58

QY 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYCNLWVFGGKTKLTVLSRTVAAPSVFIF 122
Db 59 ARFSGSGGTDFTLTITSSLEPEDFAVYICLWSSNPLTFGGGKVEI-KRTVAAPSVFIF 117

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 177

QY 183 LTLSKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 178 LTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGEC 213

RESULT 7
US-10-150-475A-4
; Sequence 4, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: 4
US-10-150-475A-4

Query Match 66.2%; Score 751; DB 14; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.8e-56;
Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;

QY 4 VVTQESA-LTTSPEGTVTLTCRSSIGAVTTSYANNVQKPDHLFTGLIGGTNNRAGVP 62
Db 3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYLQKPGQAPRIILYLTSLNLAGVP 58

QY 63 ARFSGSLIGDKAALITGAQTEDEARYFCALWYCNLWVFGGKTKLTVLSRTVAAPSVFIF 122
Db 59 ARFSGSGGTDFTLTITSSLEPEDFAVYICLWSSNPLTFGGGKVEI-KRTVAAPSVFIF 117

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 177

QY 183 LTLSKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 178 LTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGEC 213
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RESULT 8
US-10-704-522-4
; Sequence 4, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-704-522-4
Query Match 66.2%; Score 751; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.8e-56;
Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;
QY 4 VVTQESA-LTTPSGTIVTLTCRSSIGAVTTSNYANWQEKPDHLFTGLIGTNNRAGVP 62
Db 3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQKPGQAPRLLIYLTSLNLAGVP 58
QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTIVLSRTVAAPSVEIF 122
Db 59 ARFSGSGGTDTFTLTISSELEDFAVYVCLQWSSNPLTFGGGTKEI-KRTVAAPSVEIF 117
QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 177
QY 183 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 218
Db 178 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 213
RESULT 9
US-10-645-215-4
; Sequence 4, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-704-522-4
Query Match 66.2%; Score 751; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.8e-56;
Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;
QY 4 VVTQESA-LTTPSGTIVTLTCRSSIGAVTTSNYANWQEKPDHLFTGLIGTNNRAGVP 62
Db 3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQKPGQAPRLLIYLTSLNLAGVP 58
QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTIVLSRTVAAPSVEIF 122
Db 59 ARFSGSGGTDTFTLTISSELEDFAVYVCLQWSSNPLTFGGGTKEI-KRTVAAPSVEIF 117
QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 177
QY 183 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 218
Db 178 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 213
RESULT 9
US-10-645-215-4
; Sequence 4, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-704-522-4
Query Match 66.2%; Score 751; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.8e-56;
Matches 156; Conservative 13; Mismatches 41; Indels 6; Gaps 3;
QY 4 VVTQESA-LTTPSGTIVTLTCRSSIGAVTTSNYANWQEKPDHLFTGLIGTNNRAGVP 62
Db 3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQKPGQAPRLLIYLTSLNLAGVP 58
QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKTIVLSRTVAAPSVEIF 122
Db 59 ARFSGSGGTDTFTLTISSELEDFAVYVCLQWSSNPLTFGGGTKEI-KRTVAAPSVEIF 117
QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 182
Db 118 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSST 177
QY 183 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 218
Db 178 LTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 213
RESULT 10
US-09-995-693-1
; Sequence 1, Application US/09995693
; Patent No. US20020136721A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,693
; FILING DATE: 29-Nov-02 US20020136721A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,235
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1
Query Match 66.1%; Score 750; DB 9; Length 220;
Best Local Similarity 71.8%; Pred. No. 3.5e-56;
Matches 153; Conservative 13; Mismatches 43; Indels 4; Gaps 2;
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QY 9 SALTTPGCTVTLTCSRSSIGAVTTS---NYANWVQKPDHLPTGLIGGTNNRAGVPARF 65  
 Db 9 SSLTVSGEKVTVCKSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTRESGVDPDRF 68  
 QY 66 SSSLTGDKAALTTITGAQTEDEARYFCALWYCNLWVFGGCTKLTVLSTRTVAAPSVEFIFFPPS 125  
 Db 69 TGSSTGDTFTLTITSVKADDLAVYYCQYYAYPWTFFGGGTKEI-KRTVAAPSVEFIFFPPS 127  
 QY 126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT 185  
 Db 128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT 187  
 QY 186 SKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
 Db 188 SKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 11  
 US-10-232-408-1  
 ; Sequence 1, Application US/10232408  
 ; Publication No. US20030118587A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schwall, Ralph H.  
 ; Tabor, Kelly H.  
 ; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
 ; Antagonists and Uses Thereof  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Winpatin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/232,408  
 ; FILING DATE: 03-Sep-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/669,971  
 ; FILING DATE: 05-Jul-2001  
 ; APPLICATION NUMBER: US/08/952,235  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: 08/460368  
 ; FILING DATE: 02-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Marschang, Diane L.  
 ; REGISTRATION NUMBER: 35,600  
 ; REFERENCE/DOCKET NUMBER: P0938P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-5416  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 220 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-232-408-1  
 Query Match 66.1%; Score 750; DB 14; Length 220;  
 Best Local Similarity 71.8%; Pred. No. 3.5e-56;  
 Matches 153; Conservative 13; Mismatches 43; Indels 4; Gaps 2;  
 QY 9 SALTTPGCTVTLTCSRSSIGAVTTS---NYANWVQKPDHLPTGLIGGTNNRAGVPARF 65  
 Db 9 SSLTVSGEKVTVCKSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTRESGVDPDRF 68

QY 66 SSSLTGDKAALTTITGAQTEDEARYFCALWYCNLWVFGGCTKLTVLSTRTVAAPSVEFIFFPPS 125  
 Db 69 TGSSTGDTFTLTITSVKADDLAVYYCQYYAYPWTFFGGGTKEI-KRTVAAPSVEFIFFPPS 127  
 QY 126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT 185  
 Db 128 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT 187  
 QY 186 SKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
 Db 188 SKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 12  
 US-10-435-299-12  
 ; Sequence 12, Application US/10435299  
 ; Publication No. US20040052783A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weiner, George  
 ; APPLICANT: Gingrich, Roger  
 ; APPLICANT: Link, Brian  
 ; APPLICANT: Tso, J. Yun  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3  
 ; FILE REFERENCE: 05882-0176-CNUS04  
 ; CURRENT APPLICATION NUMBER: US/10/435,299  
 ; CURRENT FILING DATE: 2003-05-09  
 ; PRIOR APPLICATION NUMBER: US 09/618,380  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: US 08/397,411  
 ; PRIOR FILING DATE: 1995-03-01  
 ; PRIOR APPLICATION NUMBER: US 07/859,583  
 ; PRIOR FILING DATE: 1992-03-27  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 12  
 ; LENGTH: 213  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Complete light chain of Humanized M291 Ab  
 US-10-435-299-12

Query Match 65.7%; Score 745; DB 15; Length 213;  
 Best Local Similarity 71.2%; Pred. No. 9.1e-56;  
 Matches 153; Conservative 16; Mismatches 40; Indels 6; Gaps 3;  
 QY 5 VTQE-SALTTPGCTVTLTCSRSSIGAVTTSNYANWVQKPDHLPTGLIGGTNNRAGVPARF 63  
 Db 4 MTQSPSSLSASVGDVRVTITCSAS----SSVSYMNYQKPGKAPKRLIYDTSKLASGVPS 59  
 QY 64 REGSLIGDKAALTTITGAQTEDEARYFCALWYCNLWVFGGCTKLTVLSTRTVAAPSVEFIFF 123  
 Db 60 RFGSGSGDTFTLTITSSLPQEDFAITYCQWSSNPTFFGGGTKEI-KRTVAAPSVEFIFF 118  
 QY 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT 183  
 Db 119 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT 178  
 QY 184 TLSKADYKHKVYACEVTHQGLSXPTVTKSFNRGEC 218  
 Db 179 TLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 13  
 US-09-848-832-4  
 ; Sequence 4, Application US/09848832  
 ; Publication No. US20030165507A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hooper, Douglas  
 ; APPLICANT: Dietzschold, Bernhard  
 ; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN  
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS  
 ; FILE REFERENCE: H0001.NP0002



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 7, 2005, 15:39:10 ; Search time 25 Seconds  
(without alignments)  
839.010 Million cell updates/sec

Title: US-09-671-953B-7  
Perfect score: 1134  
Sequence: 1 RSNVQTSALTTSPGTVT.....EVTHQGLXPVTKSFNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: Pirl:.\*  
2: pirl2:.\*  
3: pirl3:.\*  
4: pirl4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	739	65.2	215	2 JE0242	Ig kappa chain NIG
2	735	64.8	215	2 JE0244	Ig kappa chain NIG
3	728.5	64.2	214	2 PC4156	Ig lambda chain V
4	721	63.6	215	2 JE0243	Ig kappa chain NIG
5	678.5	59.8	216	2 JE0241	Ig kappa chain Am3
6	672	59.3	215	2 A23746	Ig kappa chain V-I
7	578.5	51.0	135	2 S52059	JC-kappa protein -
8	549.5	48.5	240	2 S06084	Ig kappa chain pre
9	547.5	48.3	287	4 PC4402	pelB leader/Ig hea
10	544	48.0	106	1 K3HU	Ig kappa chain C r
11	541	47.7	128	2 S52450	Ig lambda chain V
12	534.5	47.1	220	2 L1M390	Ig kappa chain V r
13	533	47.0	129	1 L1M34E	Ig lambda-1 chain
14	526	46.4	235	2 S25058	Ig kappa chain - m
15	525	46.3	113	2 S06819	Ig lambda chain V
16	523.5	46.2	112	2 S06818	Ig lambda chain V
17	521	45.9	106	2 S20654	Ig lambda chain V
18	513.5	45.3	114	2 S06820	Ig kappa chain - m
19	511	45.1	219	2 S38865	Ig kappa chain - m
20	511	45.1	225	2 S37484	Ig kappa chain C r
21	509	44.9	99	2 A37927	Ig kappa chain pre
22	504.5	44.5	234	2 S14237	Ig kappa chain C r
23	503	44.4	99	2 S26653	Ig kappa chain - s
24	502.5	44.3	230	2 S33161	Ig lambda-1 chain
25	500	44.1	113	2 B54256	Ig lambda chain V
26	499.5	44.0	114	2 S06822	Ig lambda-2 chain
27	498	43.9	129	1 L2MS35	Ig kappa chain (Ma
28	497.5	43.9	214	2 S68212	Ig kappa chain V r
29	497.5	43.9	218	2 S68241	Ig kappa chain V r

30	495.5	43.7	225	2 JL0029	Ig kappa chain pre
31	495.5	43.7	234	2 S01320	Ig kappa chain pre
32	492.5	43.4	218	2 JC5810	monoclonal antibod
33	490	43.2	217	2 S42772	Ig kappa chain - m
34	488.5	43.1	99	2 PH1089	Ig lambda chain V
35	488	43.0	219	2 S16112	Ig kappa chain V r
36	486	42.9	99	2 S14582	Ig lambda chain V
37	486	42.9	113	2 S06821	Ig lambda chain V
38	485	42.8	235	2 S25749	Ig lambda chain -
39	484.5	42.7	219	2 PC4203	Ig kappa chain (no
40	478	42.2	97	2 PH1090	Ig lambda chain V
41	478	42.2	116	1 L1MSV	Ig lambda-1 chain
42	478	42.2	219	2 S52028	Ig kappa chain - m
43	473	41.7	99	2 S14584	Ig lambda chain V
44	473	41.7	100	2 PH1088	Ig lambda chain V
45	469.5	41.4	210	2 A56169	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
submitted to JIPID, November 1998  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takaashi, I.; Shinoda, A.;  
A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mu1  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 739; DB 2; Length 215;  
Best Local Similarity 70.4%; Pred. No. 1.4e-48;  
Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

QY	4	VVTQE-SALTTSPGETVLTTCRSSIGAVTTSYANVWQKPDHLFTGLIGGTTNNRAGVP	62
DB	3	VLTSQSGTSLSPGERATLSGRAS--QSVSNVLAQYQKPGQAPSLIYDASSRATGIP	60
QY	63	ARFSGSLIGDKAALITITGAQTEDEARYFCALWYCNLWVFGGKTLTVLSRTVAAPSVFIF	122
DB	61	DRFSGSGGTDFTILTISGLEPEFAVYQYQVDRPPWTFQGGTKVEI-KRTVAAPSVFIF	119
QY	123	PPSDEOLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSST	182
DB	120	PPSDEOLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSST	179
QY	183	LTLTKADYKHKYKIVACEVTHQGLSXPTKSFNRGEC	218
DB	180	LTLTKADYKHKYKIVACEVTHQGLSXPTKSFNRGEC	215

RESULT 2

JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
submitted to JIPID, November 1998  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;  
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL ar  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>



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RESULT 9
PC4402
pe1B leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion
C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C;Accession: PC4402
R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997.
A;Title: Construction, bacterial expression, and characterization of hapt-en-ep
A;Reference number: PC4402
A;Accession: PC4402
A;Molecule type: DNA
A;Residues: 1-287 <SUZ>
C;Keywords: protein

Query Match      48.3%; Score 547.5; DB 4; Length 287;
Best Local similarity 53.4%; Pred. No. 4.7e-34;
Matches 126; Conservative 14; Mismatches 49; Indels 47; Gaps 62

QY      3  AVVTQESALTTSPGETVTILTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
Db      27  AVVTQESALTTSPGETVTILTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 86
QY      63  ARPSGSLIGDKAALITGAQTEDEARFYCALWYCNLWVFGGCTKLTVLSRTVAAP-----117
Db      87  ARPSGSLIGDKAALITGAQTEDEARFYCALWYCNLWVFGGCTKLTVLSRTVAAP-----146
QY      118 -----SVFIPPSPDEQLKSG-TASVVCLLNFPYPREAKVQW-----152
Db      147  KODAKKDDAKDQGVQLQOPQGNELVPGASVKLSCKASGYFTFSYWHWVQKRPGRGLEW 206
QY      153  --KVDNALQSG-----NSQESVTEQDSKDSYTSLSSTLTLSKADYEHKKHYVAC 198
Db      207  IGRIDP--NSGGKYNEKFKSKATLTVDKPSSTAYMQLSLIT-----SEDSAVYVC 255

RESULT 10
K3HU
Ig kappa chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927;
R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.

```

Biochemistry 9, 3155-3161, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequence  
A;Reference number: A90562; MUID:71064023; PMID:5489770  
A;Contents: myeloma protein Eu  
A;Accession: B90562  
A;Molecule type: protein  
A;Residues: 1-106 <GOT>  
A;Cross-references: UNIPROT:P01934  
A;Note: This sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; Eu, disulfide bonds  
R;Suter, L.; Barnikol, H.O.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
A;Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub  
A;Reference number: A91651; MUID:72188439; PMID:5027703  
A;Contents: Bence Jones protein Ti  
A;Accession: A91651  
A;Molecule type: protein  
A;Residues: 1-106 <SUT>  
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.  
Cell 22, 197-207, 1980  
A;Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv  
A;Reference number: A90806; MUID:81042304; PMID:6775818  
A;Accession: A90806  
A;Molecule type: DNA  
A;Residues: 1-106 <HIE>  
A;Cross-references: GB:J00241; NID:G33140; PIDN:CAA23823.1; PID:G1335148  
A;Note: the sequence was determined from the germline gene  
R;Hilschmann, N.; Barnikol, H.U.; Hesser, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, A;Reference number: A94417  
A;Contents: Bence Jones protein Roy  
A;Accession: A94417  
A;Molecule type: protein  
A;Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>  
A;Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu  
R;Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
A;Title: Die voltaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).  
A;Reference number: A91639; MUID:68242259; PMID:5586923  
A;Contents: Bence Jones protein Cum  
A;Accession: A91639  
A;Molecule type: protein  
A;Residues: 1-56, 'Q', 58-106 <H12>  
R;Titani, K.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A;Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete  
A;Reference number: A92047; MUID:69234734; PMID:4893682  
A;Contents: Bence Jones protein Ag  
A;Accession: A92047  
A;Molecule type: protein  
A;Residues: 1-13, 'N', 15-106 <TIT>  
R;Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 58-59, 1970  
A;Title: Macroglobulin structure: variable sequence of light and heavy chains.  
A;Reference number: A94242; MUID:70201507; PMID:5447531  
A;Contents: Waldenström's macroglobulin Ou  
A;Accession: A94242  
A;Molecule type: protein  
A;Residues: 1-13, 'N', 15-106 <KOH>  
R;Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A;Title: Km typing with PCR: application to population screening.  
A;Reference number: A37927; MUID:91150772; PMID:1900145  
A;Accession: B37927  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 8-106 <KUR>  
A;Note: allotype Inv(3)  
R;Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987  
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A;Reference number: S02572; MUID:88005152; PMID:3115831  
A;Contents: annotation  
C;Genetics:  
A;Gene: GDB:IGKC  
A;Cross-references: GDB:120088; OMIM:147200  
A;Map position: 2p12-2p12  
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;19-88/Domain: immunoglobulin homology <IMM>  
F;26-86/Disulfide bonds: #status experimental  
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental  
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Best Local Similarity 99.1%; Pred. No. 3e-34;  
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 113 TVAAPSVFIPIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALSGNSQESVTEQDS 172  
Db 1 TVAAPSVFIPIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALSGNSQESVTEQDS 60  
Qy 173 KDSYSLSSLTLSKADYERKHVYACEVTHQGLSXPTVKSFNRGEC 218  
Db 61 KDSYSLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 106  
RESULT 11  
S52450  
Ig lambda chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S52450  
R;Berdoz, J.; Kraehenbuhl, J.P.  
submitted to the EMBL Data Library, November 1994  
A;Description: Specific amplification by the polymerase chain reaction of rearranged ge  
A;Reference number: S52445  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-128 <BER>  
A;Cross-references: EMBL:X82687; NID:G673448; PIDN:CAA58008.1; PID:G673449  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-111/Domain: immunoglobulin homology <IMM>  
Query Match 47.7%; Score 541; DB 2; Length 128;  
Best Local Similarity 96.3%; Pred. No. 6.2e-34;  
Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62  
Db 21 AVVTQESALTTSPGETVTLTCRSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 80  
Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKLTVL 110  
Db 81 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGKLTVL 128  
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A31790  
Ig kappa chain V region (17/9) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: A31790  
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an  
A;Reference number: A92686; MUID:89034213; PMID:3182835



A:Accession: A31790  
A:Molecule type: mRNA  
A:Residues: 1-220 <SCH>  
A:Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IM>

Query Match 47.1%; Score 534.5; DB 2; Length 220;  
Best Local Similarity 51.6%; Pred. NO. 3.4e-33;  
Matches 113; Conservative 26; Mismatches 75; Indels 5; Gaps 3;

QY 4 VTQEQ-SALITSPGETVTITCRSS-----IGAVTTSYANVWQKPDHLFTGLIGGTNNRAP 59  
DB 3 VMTQSPSSLITAGAEKVTMTCTSSQSLSFNSGKQKNYLTWYQKPGQPPKVLTYWASTRES 62  
QY 60 GVPARPSGLIGDKAALTTTGAQTEDEARYFCALWTCNLWVFGGQTKLTVLSRTVAAPSV 119  
DB 63 GVPDRITGSGSGDFTLITSSVQAEELANVYQNDYSNPLITFGGGTKLE-LKREDAAPTV 121  
QY 120 FIPPPDEQLKSGTASVCLLNPNFYPREAKVQKVDNALQSGNSQBSVTEQDSKSTYSYL 179  
DB 122 SIFPPSSEQLTSGASVCFVFNPNFYKDIIVKWKIDGSEKQNGVLNSWTDDQSKDSTYSM 181  
QY 180 SSTLTLSKADYEHKHYACEVTHQGLSXPKVTSFNRGEC 218  
DB 182 SSTLTLTQDEYRHNSYTCETHKTSTSPIVKSFNRNEC 220

RESULT 13  
LIMS4E  
IG lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43)  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Sep-1981 #sequence revision 24-Sep-1981 #text change 09-Jul-2004  
C:Accession: B93815; B93775; C93775; A93784; B93784; C93784; A90780; C93282; A01995  
R:Burstein, Y.; Schechter, I.  
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977  
A:Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor  
A:Reference number: A93815; MUID:77148916; PMID:403522  
A:Contents: MOPC 104E  
A:Accession: B93815  
A:Molecule type: protein  
A:Residues: 1-29 <BUR>  
A:Cross-references: UNIPROT:P01724  
A:Note: this precursor was synthesized in a cell-free system directed by messenger RNA in  
d after synthesis  
R:Appella, E.  
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971  
A:Title: Amino acid sequences of two mouse immunoglobulin lambda chains.  
A:Reference number: A93775; MUID:71107854; PMID:5276767  
A:Contents: MOPC 104E; RPC 20  
A:Accession: B93775  
A:Molecule type: protein  
A:Residues: 'Z', 21-25, 'Q', 27-129 <APP>  
A:Accession: C93775  
A:Molecule type: protein  
A:Residues: 20-129 <AP2>  
A:Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E  
R:Cesari, I.M.; Weigert, M.  
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973  
A:Title: Mouse lambda-chain sequences.  
A:Reference number: A93784; MUID:73229669; PMID:4516208  
A:Contents: J558; S104; S178  
A:Accession: A93784  
A:Molecule type: protein  
A:Residues: 20-129 <CES>  
A:Accession: B93784  
A:Molecule type: protein  
A:Residues: 20-129 <CE2>  
A:Accession: C93784  
A:Molecule type: protein  
A:Residues: 20-43, 'N', 45-70, 'N', 72-115, 'R', 117-129 <CE3>  
A:Note: these proteins were isolated from serum or urine of tumor-bearing mice

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QY 123 PPSDEQLKSTASVVCILNNFYPPEAKYQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
Db 140 PPSSEQLTSGGASVVCFLNFPYKDIYKWKIDGSEKQGVNLNSWTDQDSKSTYSMSST 199
QY 183 LTLKADYKHKVACEVTHOGLSXPTKTSFNRGEC 218
Db 200 LTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235

RESULT 15
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Ig lambda chain V region (clone 10C3) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C:Accession: S06819
R:Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A:Reference number: S06815; MUID:90064531; PMID:2555519
A:Accession: S06819
A:Molecule type: mRNA
A:Residues: 1-113 <MIL>
A:Cross-references: EMBL:X17168; NID:g52251; PID:CAA35046.1; PID:g930172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-91/Domain: immunoglobulin homology <IMM>
F:21-89/Disulfide bonds: #status predicted

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Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 1 AVVTQESALTTPSGETVTLTCRSSSTGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPGVP 60
QY 63 ARFGSLIGDKAALTITGAQTEDEARYFCALWYCNLWYFGGGTKLTVL 110
Db 61 ARFGSLIGDKAALTITGAQTEDEAIFYCSLWYSNHLVFGGGTKLTVL 108

Search completed: June 7, 2005, 16:01:08
Job time : 26 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2005, 15:37:31 ; Search time 111 Seconds  
(without alignment)  
1005.705 Million cell updates/sec

Title: US-09-671-953B-7  
Perfect score: 1134  
Sequence: 1 RSNVVTQESALTSPTGETVT.....EVTHQGLSPVTKSNRGEC 218

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	732	64.6	235	Q6GMW0	Q6gmw0 homo sapien
2	731	64.5	235	Q6P2F2	Q6pf22 homo sapien
3	728	64.2	236	Q6GMW1	Q6gmw1 homo sapien
4	725	63.9	234	Q7Z473	Q7z473 homo sapien
5	722.5	63.7	236	Q7Z3Y4	Q7z3y4 homo sapien
6	721	63.6	235	Q6GMV9	Q6gmv9 homo sapien
7	720.5	63.5	236	Q6GMX9	Q6gmx9 homo sapien
8	720.5	63.5	236	Q6PIH7	Q6pih7 homo sapien
9	719.5	63.4	236	Q6P5S8	Q6p5s8 homo sapien
10	717.5	63.3	236	Q6PIL8	Q6pil8 homo sapien
11	714.5	63.0	236	Q6GMX0	Q6gmx0 homo sapien
12	709.5	62.6	236	Q6GMX8	Q6gmx8 homo sapien
13	706.5	62.3	236	Q6PIH4	Q6pih4 homo sapien
14	699	61.6	236	Q6PIT5	Q6pit5 homo sapien
15	695	61.3	240	Q6PIH6	Q6pih6 homo sapien
16	692	61.0	239	Q8NEK0	Q8nek0 homo sapien
17	692	61.0	239	Q8TCD0	Q8tcd0 homo sapien
18	663	58.5	239	Q6P5R5	Q6p5r5 homo sapien
19	564.5	49.8	120	Q6P5R5	Q6p5r5 homo sapien
20	544	48.0	106	1 KAC_HUMAN	P01834 homo sapien
21	539	47.5	129	1 LV1E_MOUSE	P01727 mus musculus
22	534	47.1	129	1 LV1D_MOUSE	P01726 mus musculus
23	533	47.0	129	1 LV1B_MOUSE	P01724 mus musculus
24	527	46.5	129	Q8VDE2	Q8vde2 mus musculus
25	525	46.3	110	1 LV1C_MOUSE	P01725 mus musculus
26	518.5	45.7	113	Q8CGS1	Q8cgs1 mus musculus
27	516.5	45.5	238	Q6GJS7	Q6gjs7 mus musculus
28	512.5	45.2	109	Q9ET13	Q9et13 mus musculus
29	505.5	44.6	236	Q7TS98	Q7ts98 mus musculus
30	498	43.9	129	1 LV2B_MOUSE	P01729 mus musculus
31	498	43.9	219	Q65ZC0	Q65zc0 mus musculus

32	493.5	43.5	241	2	Q63ZX4	Q63zx4 mus musculus
33	478	42.2	117	1	LV1A_MOUSE	P01723 mus musculus
34	450	39.7	117	1	LV2A_MOUSE	P01728 mus musculus
35	441.5	38.9	236	2	Q8NEJ1	Q8nej1 homo sapien
36	440	38.8	235	2	Q6IN99	Q6in99 homo sapien
37	434	38.3	248	2	Q7SYU1	Q7syul xenopus lae
38	432.5	38.1	236	2	Q6IPQ0	Q6ipq0 homo sapien
39	430.5	38.0	236	2	Q6PIQ7	Q6piq7 homo sapien
40	430	37.9	233	2	Q8TBC9	Q8tbc9 homo sapien
41	428.5	37.8	230	2	Q7Z2U3	Q7z2u3 homo sapien
42	427.5	37.7	236	2	Q6GMV7	Q6gmv7 homo sapien
43	425.5	37.5	234	2	Q7Z2U7	Q7z2u7 homo sapien
44	424	37.4	231	2	Q6GNB8	Q6gnb8 xenopus lae
45	424	37.4	233	2	Q8N5F4	Q8n5f4 homo sapien

ALIGNMENTS

RESULT 1  
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ID Q6GMW0 PRELIMINARY; PRT; 235 AA.  
AC Q6GMW0;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
FAhey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073792; AAH73792.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.  
SQ . SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;  
Query Match 64.6%; Score 732; DB 2; Length 235;  
Best Local Similarity 70.3%; Pred No. 5e-56;  
Matches 154; Conservative 16; Mismatches 39; Indels 10; Gaps 5;  
Qy 4 VVTQESA-LTTSPGETVLTLCRSSIGAVTTSNTYANWVQEKPDHLFTGLIGCTNNRAPGVP 62  
Db 23 VMTQSPATLSVSPGERATLSCRAS---QSISNNLAWYQQRPGQAPRLLIYGASSRVVTGIP 79  
Qy 63 ARTSGSLIGDKAALTITGAOTDEARFYCAL---WYNLWVFGGTTKLTVLSTRTVAAPSV 119  
Db 80 GRESGSGSGTEFTLSISLQSEDPAVYFCQYNDWL--LVTFGQCTKLEI-KRTVAAPSV 136  
Qy 120 FIPPPSDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTRQDSKDSYSL 179  
Db 137 FIPPPSDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTRQDSKDSYSL 196  
Qy 180 SSTLTLSKADYKEHKVYACEVTHQGLSKPVTKSNRGEC 218  
Db 197 SSTLTLSKADYKEHKVYACEVTHQGLSSPVTKSNRGEC 235  
RESULT 2  
Q6PJF2 PRELIMINARY; PRT; 235 AA.  
AC Q6PJF2  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RT TISSUE=Lung;  
RC  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Schein J.E.,  
RA Fahy J., Halton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RC [2]  
RP SEQUENCE FROM N.A.  
RT TISSUE=Lung;  
RC  
RX Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC016380; AAH16380.1; -;  
DR HSSP; P01837; 1KCX.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; I.

DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGI; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS0835; IG LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;
Query Match	64.5%; Score 731; DB 2; Length 235;
Best Local Similarity	69.9%; Pred. No. 6.1e-56;
Matches 151; Conservative	19; Mismatches 42; Indels 4; Gaps 3
Qy	4 VVTQESA-LTTSPGETVLTICRSIGAVTTSNYANWVOEKDHLFTGLIGGTNNRAPGVP 62
Dd	23 VLTOQPATLSLSPGERATLSCRAS-QIVSSAYLAWIYQKPGQAPRLLMFGSSSRATGIP 80
Qy	63 ARFSGSLIGDKAALITIGAOTEDARFCALWYNLVFGGGTKTLTVLSRTVAAPSVEIF 122
Dd	81 DRFSGSGSDFTLTISRLEPEDFAVYCQYGSSQGTFPGTKVDI-KRTVAAPSVEIF 139
Qy	123 PPSDEQLKSGTASVVCLLNPNFYPREAKVQWKDNALSGNSQESVTEQDSKDSTYSLSST 182
Dd	140 PPSDEQLKSGTASVVCLLNPNFYPREAKVQWKDNALSGNSQESVTEQDSKDSTYSLSST 199
Qy	183 LTLISKADYEKHVKYACEVTHQGLSKPVTXSFNRGEC 218
Dd	200 LTLISKADYEKHVKYACEVTHQGLSSLPTKSFNRGEC 235
RESULT 3	
ID Q6GMW1	PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;	
DT 05-JUN-2004	(TrEMBLrel. 27, Created)
DT 05-JUL-2004	(TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
[1]	
SEQUENCE FROM N.A.	
RP TISSUE=Spleen;	
RC MEDLINE=2477932; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA Altschul S.F., Zeeberg B., Buote K.H., Schaefer C.F., Bhat N.K.,	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,	
RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerker A., Schein J.E.,	
RA Jones S.J., Marra M.A.;	
"Generation and initial analysis of more than 15,000 full-length human	
and mouse cDNA sequences."	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
[2]	
SEQUENCE FROM N.A.	
RP TISSUE=Spleen;	
RC Strausberg R.;	
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
RL EMBL; BC073791; AAH73791.1; -.	
DR InterPro; IPR003599; Ig.	
DR InterPro; IPR007110; Ig-like.	

DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS08335; IG-LIKE; 2.  
DR PROSITE; PS0290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 64.2%; Score 728; DB 2; Length 236;  
Best Local Similarity 70.0%; Pred. No. 1.1e-55;  
Matches 154; Conservative 15; Mismatches 45; Indels 6; Gaps 4;  
QY 1 RSAV-VTQE-SALTTPSGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRA 58  
DB 21 RCAIQTQSPSSLSASVGRVITCRASQ---ISNDLGMVQKPKAPKLIIYAASSLIQ 77  
QY 59 PGVPARFSGSLIGDKAALITGAGTQDEARFPCALWYCNLVWFGGKTLTVLSRTVAAPS 118  
DB 78 SGVPSRFGSGSGTDFTLTISSLPQEDFATYICLDYNYPTWTFGQGTKEI-KRTVAAPS 136  
QY 119 VFIPPSDEQLSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDYTS 178  
DB 137 VFIPPSDEQLSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDYTS 196  
QY 179 LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218  
DB 197 LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 236

## RESULT 4

Q72473 ID Q72473 PRELIMINARY; PRT; 234 AA.  
AC Q72473;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;

RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBAJ databases.  
DR EMBL; BC056256; AAH56256.1; --  
DR HSP; P01834; 1HEZ.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS08335; IG-LIKE; 2.  
DR PROSITE; PS0290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 63.9%; Score 725; DB 2; Length 234;  
Best Local Similarity 68.2%; Pred. No. 2e-55;  
Matches 150; Conservative 19; Mismatches 45; Indels 6; Gaps 4;  
QY 1 RSAV-VTQE-SALTTPSGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGTNNRA 58  
DB 19 RCAIQTQSPSSLSASVGRVITCRAS---QSIGSLAWYQKPKAPKLIIYAASSLIQ 75  
QY 59 PGVPARFSGSLIGDKAALITGAGTQDEARFPCALWYCNLVWFGGKTLTVLSRTVAAPS 118  
DB 76 SGVPSRFGSGSGTDFTLTISSLPQEDFATYICLDYNYPTWTFGQGTKEI-KRTVAAPS 134  
QY 119 VFIPPSDEQLSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDYTS 178  
DB 135 VFIPPSDEQLSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDYTS 194  
QY 179 LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218  
DB 195 LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234

## RESULT 5

Q723Y4 ID Q723Y4 PRELIMINARY; PRT; 236 AA.  
AC Q723Y4;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;

Proc. Natl. Acad. Sci. U.S.A.	99:16899-16903 (2002).
SEQUENCE FROM N.A.	
TISSUE=Spleen;	
Strausberg R.;	
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
EMBL; BC073793, AAH73793.1; -	
InterPro; IPR003599; IG.	
InterPro; IPR007110; IG-like.	
InterPro; IPR003597; IG.cl.	
InterPro; IPR003006; IG_MHC.	
InterPro; IPR003596; IG_v.	
Pfam; PF07654; C1-set; 1.	
Pfam; PF00047; IG; 2.	
SMART; SM00409; IG; 2.	
SMART; SM00407; IGcl; 1.	
SMART; SM00406; IGv; 1.	
PROSITE; PS00835; IG_LIKE; 2.	
PROSITE; PS00290; IG_MHC; UNKNOWN_1.	
Hypothetical protein.	
SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;	
Query Match	63.6%; Score 721; DB 2; Length 235;
Best Local Similarity	69.4%; Pred. No. 4.6e-55;
Matches 150; Conservative 15; Mismatches 47; Indels 4; Gaps 3;	
QY 4 VTQE-SALTTPGETVTITCRSSIGAVTTSYANVWQKPDHLFTGLIGGTNNRAGVP 62	
DB 23 VLTFQSGTUSLSPGERAAUSCRAS--QSNVSKYLAWYQKPGQAPRLMYAASIRATGIP 80	
QY 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWCNIVWFGGGTKLTVLSRTVAAPSVFIF 122	
DB 81 DRFGSGSGGTDTLTITSRLESEDFALYFCQYGTGTSPLTFGGGTKEI-KRTVAAPSVFIF 139	
QY 123 PPSDEQLKSGTASVVCLLNNFPYREAKVQKVDNALQSGNSQBSVTEQDSKDSYLSST 182	
DB 140 PPSDEQLKSGTASVVCLLNNFPYREAKVQKVDNALQSGNSQBSVTEQDSKDSYLSST 199	
QY 183 LTLSKADYEKKHYACVETHVTHQGLSXSVTKSFNRGEC 218	
DB 200 LTLSKADYEKKHYACVETHVTHQGLSXSVTKSFNRGEC 235	
RESULT 7	
Q6GMX9 PRELIMINARY; PRT; 236 AA.	
ID Q6GMX9	
AC Q6GMX9	
DT 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE Hypothetical protein.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Primary B-Cells;	
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,	
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,	
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,	
RA Diatchenko L., Marustina K., Farmer A.A., Rubin G.M., Hong L.,	
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,	
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF77 CRC64;

Query Match 63.5%; Score 720.5; DB 2; Length 236;
Best Local Similarity 69.3%; Pred. No. 5.1e-55;
Matches 149; Conservative 17; Mismatches 44; Indels 5; Gaps 3;

QY 5 VTQE-SALTSPGETVTLTCRSSIGAVTTSYANVWQEKPDHLFTGLIGGTNNRPGVPA 63
DB 26 MTQSPSLSASVGHRTVITCRAS---QNVSRWLAWYQORPEKAPKSLIVATSSLSHGVP 82

QY 64 RFGSLIGDKAALTITGAOTEDARYFCALWYCNLWVFGGTKLTVLSRTVAAPSVFI 123
DB 83 RFGSGSGDTFTLITSSLPQEDPATYICQYNTYPLTFGGTKVEI-KRTVAAPSVFI 141

QY 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 183
DB 142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 201

QY 184 TLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 218
DB 202 TLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 236

RESULT 8
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 63.5%; Score 720.5; DB 2; Length 236;
Best Local Similarity 70.2%; Pred. No. 5.1e-55;
Matches 151; Conservative 15; Mismatches 44; Indels 5; Gaps 3;

QY 5 VTQE-SALTSPGETVTLTCRSSIGAVTTSYANVWQEKPDHLFTGLIGGTNNRPGVPA 63
DB 26 LTQSPSLSASVGHRTVITCRASQ---ISSYLAWYQKPKAPNLLIYAASLTQSGVPS 82

QY 64 RFGSLIGDKAALTITGAOTEDARYFCALWYCNLWVFGGTKLTVLSRTVAAPSVFI 123
DB 83 RFGSGSGDTFTLITSSLPQEDPATYICQYNTYPLTFGGTKVEI-KRTVAAPSVFI 141

QY 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 183
DB 142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 201

QY 184 TLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 218
DB 202 TLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 236

RESULT 9
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Straubeberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4F5F27 CRC64;
Query Match 63.4%; Score 719.5; DB 2; Length 236;
Best Local Similarity 69.6%; Pred. No. 6.3e-55;
Matches 151; Conservative 17; Mismatches 44; Indels 5; Gaps 4;
Qy 4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNANWQEKPDHLFTGLIGTNNRAPGVP 62
Db 23 VLTQSPGTLSPGERATLSCRAS--QTVFSSHLAWYQORPGQAPRLIYGVSSRATGIP 80
Qy 63 ARFSGSLIGDKAALITIGAQTEDEARFYFCALWYCN-LWVFGGKTLVLSRTVAAPSVFI 121
Db 81 DRFSGSGSGTDFTLTITRLEPEDFAVYFCQYQYGTSPSLTFGGGTRVEI-KRTVAAPSVFI 139
Qy 122 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 181
Db 140 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 199
Qy 182 TLTLKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 200 TLTLKADYKHKVYACEVTHQGLSSPTKSFNRGEC 236
RESULT 10
Q6PIL8 PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Straubeberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;
Query Match 63.3%; Score 717.5; DB 2; Length 236;
Best Local Similarity 69.6%; Pred. No. 9.4e-55;
Matches 151; Conservative 18; Mismatches 43; Indels 5; Gaps 4;
Qy 4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNANWQEKPDHLFTGLIGTNNRAPGVP 62
Db 23 VLTQSPGTLSPGERATLSCRAS--QSLSSYLAWYQKPGQAPRLIYGVSSRATGIP 80
Qy 63 ARFSGSLIGDKAALITIGAQTEDEARFYFCALWYCNLWV-FGGGKTLVLSRTVAAPSVFI 121
Db 81 DRFSGSGSGTDFTLTITRLEPEDFAVYFCQYQYGTSPITFGGTRLDI-KRTVAAPSVFI 139
Qy 122 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 181
Db 140 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSS 199
Qy 182 TLTLKADYKHKVYACEVTHQGLSXPTKSFNRGEC 218
Db 200 TLTLKADYKHKVYACEVTHQGLSSPTKSFNRGEC 236
RESULT 11
Q6GMX0 PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RA Strausberg R.;  
DR EMBL; BC073775; AAH73775.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;  
Query Match 63.08; Score 714.5; DB 2; Length 236;  
Best Local Similarity 69.3%; Pred. No. 1.7e-54;  
Matches 149; Conservative 16; Mismatches 45; Indels 5; Gaps 3;  
QY 5 VTQE-SALTTSPEETVLTCSRSGVATTSTNYANWVQEKPDHLFTGLIGTNNRAPGVA 63  
Db 26 MTQSPSLASVGDRTVITCRAS---QNINYNLWYQKFGKAPNLLIYAASLSQGVPS 82  
QY 64 RFGSLIGDKAALTITGAOTEDEARFYCALWYCNLWVFGGGTKLTVLSRTVAAPSVEIFP 123  
Db 83 RFGSGSGDFTLTITSSLRPDDFATYYCQOSINPLTFGGGTNVEI-KRTVAAPSVEIFP 141  
QY 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL 183  
Db 142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL 201  
QY 184 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 202 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 236  
RESULT 12  
Q6GMX8 PRELIMINARY; PRT; 236 AA.  
ID Q6GMX8  
AC Q6GMX8  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RA Strausberg R.;  
DR EMBL; BC073764; AAH73764.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559BFC9 CRC64;  
Query Match 62.6%; Score 709.5; DB 2; Length 236;  
Best Local Similarity 68.8%; Pred. No. 4.7e-54;  
Matches 148; Conservative 19; Mismatches 43; Indels 5; Gaps 3;  
QY 5 VTQE-SALTTSPEETVLTCSRSGVATTSTNYANWVQEKPDHLFTGLIGTNNRAPGVA 63  
Db 26 MTQSPSLASVGDRTVITCRASQ---ISSWLAWYQKFGKAPKLLIYAASLSQGVPS 82  
QY 64 RFGSLIGDKAALTITGAOTEDEARFYCALWYCNLWVFGGGTKLTVLSRTVAAPSVEIFP 123  
Db 83 RFGSGSGDFTLTITSSLRPDDFATYYCQOAHSPFTFGTGVDI-KRTVAAPSVEIFP 141  
QY 124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL 183  
Db 142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL 201  
QY 184 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218  
Db 202 TLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 236

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RESULT 13
QSPH4 PRELIMINARY; PRT; 236 AA.
ID Q6PIH4
AC Q6PIH4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06E8E26 CRC64;

Query Match 62.3%; Score 706.5; DB 2; Length 236;
Best Local Similarity 68.8%; Pred. No. 8.7e-54;
Matches 148; Conservative 18; Mismatches 44; Indels 5; Gaps 3;

QY 5 VTQE-SALTTSQGEVTLTCRSGIGAVTTSNYANVQEKPDHLFTGLIGGTNNRAGVPA 63
DB 26 MTQSTSLASVGDRTVITACRAS---QWISDLAWYQKPGKAPKLLIYDASRLSGVPS 82
QY 64 RFGSLIGDKAALTITGAQTEDEARYFCALWYFCALWVFGGKTLVLSRTVAAPSVFIFF 123
DB 83 RFGSGSGTFSLTISGLQPDFFARYYCOPYNSPQFGQTKVEI-KRTVAAPSVFIFF 141
QY 124 PSEDLKSGTASVCLNLFYPREAKVQMKVDNALQSGNSQBSVTEQDSKSTYLSSTL 183
DB 142 PSEDLKSGTASVCLNLFYPREAKVQMKVDNALQSGNSQBSVTEQDSKSTYLSSTL 201

184 TLSKADYEKKHKYACEVTHQGLSXPTKSNRGC 218
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202 TLSKADYEKKHKYACEVTHQGLSPVTKSNRGC 236
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RESULT 14
Q6PIT5 PRELIMINARY; PRT; 236 AA.
ID Q6PIT5
AC Q6PIT5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029444; AAH29444.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEEB351 CRC64;

Query Match 61.6%; Score 699; DB 2; Length 236;
Best Local Similarity 68.6%; Pred. No. 3.9e-53;
Matches 151; Conservative 15; Mismatches 48; Indels 6; Gaps 4;

QY 1 RSVA-VTQE-SALTTSQGEVTLTCRSGIGAVTTSNYANVQEKPDHLFTGLIGGTNNRA 58
DB 21 RCATLQTSPLSLSVSGERVITICRASQG---ISSALAWYQKPGKPKLLIYDASTME 77
QY 59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYFCALWVFGGKTLVLSRTVAAPS 118
|||||
78 SGVPSRPSFGSGSGTHFTLTITSSLOPEDPATFYCQOFKSPYRPTFGQGTTLLEI-KRTVAAPS 136
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30	SLSVTPGEPASISCRSSOSLHSGNYNFDWYLOKPCQSPOLLIIWGSNRPASGVDPDFSG	89
68	SLIGDKAALTTTGAQTEDEARYFC--ALWYCNLWVFGGGKTLTVLSRTVAAPSVFIPPPS	125
90	SGSGTDFTLKISRVEAEVDGVYCMQAL-QTPPYTFGGTKLEI-KETVAAPSVFIPPPS	147
126	BDQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKDSYLSSTLT	185
148	BDQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKDSYLSSTLT	207
186	SKADYEKKHKVACEVTHOGLSKPYTKFSNRCG	218
208	SKADYEKKHKVACEVTHOGLSPYTKFSNRCG	240

Search completed: June 7, 2005, 16:00:12  
Job time : 112 secs

119	QY	VFI	PPSPDEQLKSGTASVVCLLNNFY	PREAKVQWKVNALQSGNSQESVTEQDSKOSTYS	178
120					
121					
122					
123	DB	VFI	PPSPDEQLKSGTASVVCLLNNFY	PREAKVQWKVNALQSGNSQESVTEQDSKOSTYS	196
124					
125					
126					
127	QY	LS	STLTLKADYERKHVYACEVTHQGLSX	PVTKSFNRGEC	218
128					
129					
130	DB	LS	STLTLKADYERKHVYACEVTHQGLSX	PVTKSFNRGEC	236
131					
132					
133					

RESULT 15

Q6PIH6	PRELIMINARY;	PRT;	240 AA.		
ID					
AC	Q6PIH6;				
CD	05-PIH-2004 (TrEMBLrel. 27, Created)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)				
DE	Hypothetical protein.				
DE	Homo sapiens (Human).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	TISSUE=Lung;				
RX	MEDLINE=123288257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T.I., Wang J., Hsieh F.,				
RA	Platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzyszynski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
PL	Proc Natl Acad Sci U S A. 99:16899-16903(2002).				

[2] **SEQUENCE FROM N.A.**  
**RC** TISSUE=Lung;  
**RA** Strauberg R.;  
**RL** Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
**EMBL**; BC034142; AAH34142.1; -.  
**DR** HSSP; P01837; 1KB5.  
**DR** InterPro; IPR003599; IG.  
**DR** InterPro; IPR007110; IG-like.  
**DR** InterPro; IPR003597; IG cl.  
**DR** InterPro; IPR003006; IG\_MHC.  
**DR** InterPro; IPR003596; IG\_v.  
**DR** Pfam; PF07654; Cl-sec; 1.  
**DR** SMART; SM00409; IG; 2.  
**DR** SMART; SM00407; IGcl; 1.  
**DR** SMART; SM00406; IGv; 1.  
**DR** PROSITE; PS50835; IG\_LIKE; 2.  
**DR** PROSITE; PS00290; IG\_MHC; 1.  
**DR** PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
**DR** Hypothetical protein.  
**KO** SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

[illegible]

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